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could you run a regular search and an interference search on seq id 1 and 2

thanks

Christopher Yaen
US Patent Office
Art Unit 1642
571-272-0838
REM 3A20
REM 3C18

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OM protein - protein search, using sw model

Run on: August 16, 2004, 11:08:06 ; Search time 50.4574 Seconds
(without alignments)
649.568 Million cell updates/sec

Title: US-09-889-300A-1

Perfect score: 614

Sequence: 1 QVQLQQSGAELVRPGTSVKV.....ARDGPWFYWGQGLTVTSA 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

- 1: Geneseqpl980s.*
- 2: Geneseqpl990s.*
- 3: Geneseqpl2000s.*
- 4: Geneseqpl2001s.*
- 5: Geneseqpl2002s.*
- 6: Geneseqpl2003as.*
- 7: Geneseqpl2003bs.*
- 8: Geneseqpl2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	116	3 AAB10443	Aab10443 Murine mo
2	554.5	90.3	119	2 AAW49814	Aaw49814 Amino aci
3	554.5	90.3	119	6 ABR55869	Abr55869 Anti-glyc
4	554.5	90.3	138	2 AAR39266	Aar39266 Mouse C4g
5	554.5	90.3	138	2 AAW49810	Aaw49810 Variable
6	546.5	89.0	119	2 AAW01580	Aaw01580 Lead bind
7	519	84.5	138	6 AAE34367	Aae34367 Escherich
8	517.5	84.3	164	5 ABG71533	Abg71533 Mouse ant
9	515	83.9	137	2 AAR12360	Aar12360 Heavy cha
10	515	83.9	137	2 AAR12238	Aar12238 Mouse MAB
11	515	83.9	141	2 AAR09427	Aar09427 ME4 Heavy
12	515	83.9	141	2 AAW06216	Aaw06216 MAB ME4 h
13	515	83.9	141	2 AAW85063	Aaw85063 Mouse ME4
14	515	83.9	141	6 ABUS5897	Abus5897 Mouse ant
15	510.5	83.1	138	2 AAW34515	Aaw34515 Variable
16	503.5	82.0	119	2 AAW49813	Aaw49813 Amino aci
17	503.5	82.0	121	2 AAW07437	Aaw07437 Anti-DNA
18	503.5	82.0	222	2 AAR39267	Aar39267 Humanised
19	503.5	82.0	222	2 AAW49817	Aaw49817 Fragment
20	503.5	82.0	235	2 AAR39268	Aar39268 Humanised
21	503.5	82.0	235	2 AAW49818	Aaw49818 Amino aci
22	503.5	82.0	235	2 ABR55871	Abr55871 Human inm
23	503.5	82.0	448	6 ABR55871	Abr55871 Human inm
24	503.5	82.0	449	2 AAR43339	Aar43339 Completel
25	503.5	82.0	449	2 AAW49816	Aaw49816 Amino aci

26	502.5	81.8	164	5 ABG71534	Abg71534 Mouse ant
27	498.5	81.2	136	1 AAP70624	Aap70624 Sequence
28	498.5	81.2	136	2 AAW10239	Aaw10239 Chimeric
29	498.5	81.2	136	2 AAW10584	Aaw10584 Anti-hepa
30	498.5	81.2	136	2 AAW16340	Aaw16340 Mouse-hum
31	498.5	81.2	136	2 AAW41054	Aaw41054 Human ant
32	498.5	81.2	136	2 AAW47510	Aaw47510 Human ant
33	498.5	81.2	136	2 AAW47517	Aaw47517 Human ant
34	498.5	81.2	136	2 AAW89535	Aaw89535 Chimeric
35	498.5	81.2	136	4 AAB98085	Abc98085 Chimeric
36	498.5	81.2	136	7 ADC65003	Adc65003 Human inm
37	497.5	81.0	117	2 AAR88716	Aar88716 Mouse ant
38	497.5	81.0	166	5 ABG71536	Abg71536 Mouse ant
39	497.5	81.0	574	7 ADE52216	Ades2216 E3Bi prot
40	497.5	81.0	2606	7 ADE52217	Ades2217 PG1EN-EH3
41	497.5	81.0	2606	7 ADE52214	Ades2214 PG1EN-EH3
42	492	80.1	272	2 AAW00557	Aaw00557 Nematode
43	492	80.1	272	2 AAW43913	Aaw43913 Mus muscu
44	490.5	79.9	119	2 AAW01585	Aaw01585 Lead bind
45	490.5	79.9	121	2 AAW00833	Aaw00833 Variable

ALIGNMENTS

RESULT 1

AAB10443

ID AAB10443 standard; protein; 116 AA.

XX AAB10443;

AC AAB10443;

XX 01-DEC-2000 (first entry)

DE Murine monoclonal antibody MAK HE2 variable region heavy chain.

KW Murine; monoclonal antibody; MAK HE2; heavy chain; variable region;

KW human cellular membrane antigen; tumor associated antigen; TAA; vaccine;

XX cancer.

XX Mus sp.

XX WO200041722-A1.

XX 20-JUL-2000.

XX 12-JAN-2000; 2000WO-EP000174.

XX 13-JAN-1999; 99CH-000000051.

XX (IGEN-) IGENEON GMBH.

XX Eckert H, Loibner H;

XX WPI; 2000-475956/41.

XX Novel use of antibodies against human cellular membrane antigens for

XX vaccination against cancer.

XX Example 3; Page 47; 54pp; German.

XX This invention describes the novel use of an antibody targeted to a human

XX cellular membrane antigen, to manufacture a medicament to

XX prophylactically and/or therapeutically vaccinate against cancer. The

XX antibodies against tumor associated antigen (TAA) for prophylactic and/or

XX compared to antibodies against TAA for passive immunotherapy), typically

XX less than 1 mg by injection. The antibodies also have a long continual

XX activity that directly induces immunity and their shelf life is unlimited

XX (fresh vaccination is always possible). This sequence represents the

XX murine monoclonal antibody MAK HE2 variable region heavy chain fragment

XX which is used in the method of the invention

XX Sequence 116 AA;

Query Match 100.0%; Score 614; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 8e-47; Mismatches 0; Indels 0; Gaps 0;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGAELVRPQTSVKVSKASGYAFTNYLIIEWVKQRPQGLEWIGVINPGSGGTNY 60
DB 1 QVQLQSGAELVRPQTSVKVSKASGYAFTNYLIIEWVKQRPQGLEWIGVINPGSGGTNY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSSAVYFCARDGFWPAYWGQGLTVTUSA 116
DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSSAVYFCARDGFWPAYWGQGLTVTUSA 116

RESULT 2
AAW49814
ID AAW49814 standard; protein; 119 AA.
XX AC AAW49814;
XX 25-MAR-2003 (revised)
XX 24-SEP-1998 (first entry)
XX Amino acid sequence of the mouse antibody C4G1 mature heavy chain.
XX Heavy chain; humanised; immunoglobulin; Ig; mouse C4G1; antibody;
XX inhibition; antigen; cardiovascular disease; thromboembolic disorder;
XX cancer; acute myocardial infarction; unstable angina; stroke;
XX transient ischemic episode; pulmonary embolism; deep vein thrombosis;
XX extracorporeal cardiopulmonary circulation.

XX OS Mus sp.
XX FH Key
XX Domain 31..35
XX Location/Qualifiers
XX /note="complementarity determining region"
XX Domain 50..56
XX /note="complementarity determining region"
XX Domain 99..108
XX /note="complementarity determining region"
XX US5777085-A.
XX PN
XX 07-JUL-1998.
XX DD
XX 17-MAY-1995; 95US-00458516.
XX PF
XX 20-DEC-1991; 91US-00812111.
XX PR 09-JUN-1992; 92US-00895952.
XX PR 11-SEP-1992; 92US-00944159.
XX PR 03-MAY-1993; 93US-00059159.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX (YAMA) YAMANOUCHI PHARM CO LTD.
XX PA
XX Tso JY, Co MS;
XX PI
XX WPI; 1998-398136/34.
XX DR
XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse
XX C4G1 antibody, used for inhibiting platelet aggregation for treating
XX cardiovascular and thromboembolic disorders.
XX Claim 1; Fig 5B; 35pp; English.
XX PS
XX This is the amino acid sequence of the humanised antibody C4G1 heavy
XX chain, used in the method of the invention involving the creation of a
XX humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody. The
XX humanised Ig is capable of binding to GPIIb/IIIa and inhibiting platelet
XX aggregation and also the releasing reaction of platelets. The Ig can be
XX used for treating cardiovascular diseases and thromboembolic disorders,
XX e.g. acute myocardial infarction, unstable angina, stroke, transient
XX ischemic episodes, deep vein thrombosis and pulmonary embolism,

CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
CC diagnosing the presence and location of a thrombus, or certain types of
CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
CC detection of GPIIb/IIIa antigens or for isolating platelets. (Updated on
CC 25-MAR-2003 to correct PA field.)
XX SQ Sequence 119 AA;
XX Query Match 90.3%; Score 554.5; DB 2; Length 119;
XX Best Local Similarity 91.6%; Pred. No. 1.5e-41;
XX Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;
QY 1 QVQLQSGAELVRPQTSVKVSKASGYAFTNYLIIEWVKQRPQGLEWIGVINPGSGGTNY 60
DB 1 QVQLQSGAELVRPQTSVKVSKASGYAFTNYLIIEWVKQRPQGLEWIGVINPGSGGTNY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSSAVYFCA-RDG--PWFAYWGQGLTVTUSA 116
DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSSAVYFCARDGNYGWFAYWGQGLTVTUSA 119

RESULT 3
ABR55869
ID ABR55869 standard; protein; 119 AA.
XX AC ABR55869;
XX 02-SEP-2003 (first entry)
XX Anti-glycoprotein IIb/IIIa Mab mature heavy chain variable region.
XX Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;
XX glycoprotein IIb/IIIa; monoclonal antibody; human; antibody.
XX Mus musculus.
XX WO2003031464-A2.
XX 17-APR-2003.
XX 09-OCT-2002; 2002WO-US032263.
XX 10-OCT-2001; 2001US-0328523P.
XX 19-OCT-2001; 2001US-0344692P.
XX 28-NOV-2001; 2001US-0334233P.
XX 28-NOV-2001; 2001US-0334301P.
XX 07-JUN-2002; 2002US-0387292P.
XX 25-JUN-2002; 2002US-0391777P.
XX 17-JUL-2002; 2002US-0396594P.
XX 16-AUG-2002; 2002US-0404249P.
XX 28-AUG-2002; 2002US-0407527P.
XX (NEOS-) NEOSE TECHNOLOGIES INC.
XX PA
XX De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX WPI; 2003-449162/42.
XX DR
XX Remodeling a peptide, by removing a saccharyl subunit from the peptide to
XX form truncated glycan, and adding or deleting glycosyl groups to a
XX peptide and/or adding modifying group of a peptide to remodel the
XX peptide.
XX Example; Fig 77; 900pp; English.
XX PS
XX The invention relates to a cell-free, in vitro method of remodeling a
XX peptide. The method involves removing a saccharyl subunit from the
XX peptide, thus forming a truncated glycan, and contacting the truncated
XX glycan with at least one glycosyltransferase and at least one glycosyl
XX donor under conditions suitable to transfer at least one glycosyl donor
XX to the truncated glycan, thus remodeling the peptide. Conjugates can be
XX formed between a granulocyte colony stimulating factor (G-CSF) peptide,
XX interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,

CC Factor IX peptide, follicle stimulating hormone peptide, erythropoietin
CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)
CC peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI)
CC peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)
CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha
CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-
CC glycoprotein IIB/IIIA monoclonal antibody peptide, chimeric anti HER2
CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-
CC CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,
CC insulin peptide, hepatitis B surface antigen (HbsAg), human growth
CC hormone (HGH) peptide, and a modifying group, where the modifying group
CC is covalently attached to the peptide through an intact glycosyl linking
CC group. The method is useful for a cell-free, in vitro method of
CC remodeling the above mentioned peptides. The present sequence represents
CC an anti-glycoprotein IIB/IIIA monoclonal antibody mature heavy chain
XX variable region
XX
SQ Sequence 119 AA;

Query Match 90.3%; Score 554.5; DB 6; Length 119;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

QY 1 QVQLQSGAELVRGTSVKVSKASGYAFNTYLLIEWVKORPGQGLEWIGVINPGSGGTNY 60
DB 1 QVQLQSGAELVPGTSVRVSKASGYAFNTYLLIEWVKORPGQGLEWIGVINPGSGGTNY 60
QY 61 NEKFKGKATLTADKSSSTAYWQLSSLTSDSAVFCA-RDG--PWFAYWGQGLTVTVA 116
DB 61 NEKFKGKATLTVDKSSSTAYWQLSSLTSDSAVFCA-RDGDGNYGWFAYWGRGTLTVTVA 119

RESULT 4
AAR39266
ID AAR39266 standard; protein; 138 AA.
XX
AC AAR39266;
XX
DT 25-MAR-2003 (revised)
DT 29-NOV-1993 (first entry)
XX
DE Mouse C4G1 Ig heavy-chain.
XX
KW Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIb/IIIb;
KW monoclonal antibody; platelet agglutination; humanised antibody.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /label= signal_peptide
FT /label= light_chain
FT Region 21..138
FT /label= light_chain
FT Region 50..54
FT /label= complementarity_determining_region_1
FT Region 69..85
FT /label= CDR_2
FT Region 118..127
FT /label= CDR_3
XX WO9313133-A1.
XX
XX 08-JUL-1993.
XX
XX 15-DEC-1992; 92WO-JP001630.
XX
XX 20-DEC-1991; 91US-00812111.
PR 09-JUN-1992; 92US-00895952.
PR 11-SEP-1992; 92US-00944159.
XX
XX (YAMA) YAMANOUCHI PHARM CO LTD.
PA (PROT-) PROTEIN DESIGN LABS INC.
XX

PI Co MS, Tso JY;
XX
DR WPI; 1993-227275/28.
DR N-PSDB; AAQ45663.
XX
XX Compn. contg. immunoglobulin specific for the GP-IIb and -IIIA protein -
XX for treating disorders related to vascular thrombosis.
PS Disclosure; Fig 2B; 54pp; Japanese.
XX
XX This is the sequence of the mouse C4G1 immunoglobulin heavy chain. See
CC AAR39265 for the light chain sequence. The antibody is specific for the
CC GPIIb/IIIb protein and inhibits platelet agglutination. The Ig is thus
CC useful in the treatment of thrombosis. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 138 AA;

Query Match 90.3%; Score 554.5; DB 2; Length 138;
Best Local Similarity 91.6%; Pred. No. 1.8e-41;
Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

QY 1 QVQLQSGAELVRGTSVKVSKASGYAFNTYLLIEWVKORPGQGLEWIGVINPGSGGTNY 60
DB 20 QVQLQSGAELVGGTSVRVSKASGYAFNTYLLIEWVKORPGQGLEWIGVINPGSGGTNY 79
QY 61 NEKFKGKATLTADKSSSTAYWQLSSLTSDSAVFCA-RDG--PWFAYWGQGLTVTVA 116
DB 80 NEKFKGKATLTVDKSSSTAYWQLSSLTSDSAVFCA-RDGDGNYGWFAYWGRGTLTVTVA 138

RESULT 5
AAW49810
ID AAW49810 standard; protein; 138 AA.
XX
AC AAW49810;
XX
DT 25-MAR-2003 (revised)
DT 24-SEP-1998 (first entry)
XX
DE Variable region of mouse antibody C4G1 light chain.
XX
KW Mouse; antibody C4G1; heavy chain; humanised; immunoglobulin; Ig;
KW inhibition; antigen; cardiovascular disease; thromboembolic disorder;
KW cancer; acute myocardial infarction; unstable angina; stroke;
KW transient ischemic episode; pulmonary embolism; deep vein thrombosis;
KW extracorporeal cardiopulmonary circulation.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein 20..138
FT /note= "mature protein"
FT Domain 50..54
FT /note= "complementarity determining region"
FT Domain 69..85
FT /note= "complementarity determining region"
FT Domain 118..127
FT /note= "complementarity determining region"
XX US5777085-A.
XX
XX 07-JUL-1998.
XX
XX 17-MAY-1995; 95US-00458516.
XX
XX 20-DEC-1991; 91US-00812111.
PR 09-JUN-1992; 92US-00895952.
PR 11-SEP-1992; 92US-00944159.
PR 03-MAY-1993; 93US-00059159.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
PA

PA (YAMA) YAMANOUCHI PHARM CO LTD.

PI Tso JY, Co MS;

XX WPI; 1998-398136/34.

DR N-PSDB; AAV36742.

XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse
PT C4G1 antibody, used for inhibiting platelet aggregation for treating
PT cardiovascular and thromboembolic disorders.

XX Disclosure; Fig 2B; 35pp; English.

XX This is the amino acid sequence of the mouse antibody C4G1 heavy chain,
CC used in the method of the invention involving the creation of a humanised
CC immunoglobulin (Ig) derived from the mouse C4G1 antibody. The humanised
CC Ig is capable of binding to GPIIb/IIIa and inhibiting platelet
CC aggregation and also the releasing reaction of platelets. The Ig can be
CC used for treating cardiovascular diseases and thromboembolic disorders,
CC e.g. acute myocardial infarction, unstable angina, stroke, transient
CC ischemic episodes, deep vein thrombosis and pulmonary embolism,
CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
CC diagnosing the presence and location of a thrombus, or certain types of
CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
CC detection of GPIIb/IIIa antigens or for isolating platelets. (Updated on
CC 25-MAR-2003 to correct PA field.)

XX Sequence 138 AA;

Query Match 90.3%; Score 554.5; DB 2; Length 138;
Best Local Similarity 91.8%; Pred. No. 1.8e-41; Indels 3; Gaps 2;
Matches 109; Conservative 3; Mismatches 4;

QY 1 QVQLQSGAELVRFGTSVKVSCKASGYAFTNYLIEWVKQRPQGLEWIGVINPGSGGTNY 60

DB 20 QVQLQSGAELVRFGTSVKVSCKASGYAFTNYLIEWVKQRPQGLEWIGVINPGSGGTNY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCA-RDG---PWFAYWGQGLTVTVSA 116

DB 80 NEKFKGKATLTVDKSTTAYMQLSSLTSDSAVYFCARRDGNVGFAYWGRGTLTVTVSA 138

RESULT 6

ID AAW01580 standard; protein; 119 AA.

AC AAW01580;

XX 22-AUG-1997 (first entry)

XX Lead binding MAB 14F11 heavy chain variable region.

XX Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
XX heavy metal.

OS Mus musculus.

XX W09639518-A1.

XX 12-DEC-1996.

XX 05-JUN-1996; 96WO-US009258.

XX 05-JUN-1995; 95US-00462798.

XX 10-OCT-1995; 95US-00541373.

XX (BION-) BIONEERASKA INC.

XX Wylie DE, Lopez O, Murray PJ;

XX WPI; 1997-043140/04.

DR N-PSDB; AAT58254.

XX

PT DNA encoding heavy metal binding polypeptide sequences - used for
PT detecting, removing, adding or neutralising heavy metals, such as lead
PT cations.

XX Claim 12; Page 63; 125pp; English.

XX

CC The present sequence represents the heavy chain variable region for
CC monoclonal antibody (Mab) 14F11, which immunoreacts with a lead cation.
CC The sequence was derived from RNA isolated from mouse hybridoma cells.
CC The protein can be used for binding heavy metals, such as lead cations.
CC It can be used for detecting, removing, adding or neutralising the heavy
CC metals in biological and inanimate systems. It can be used in e.g.
CC aqueous liquid systems, in biological or environmental systems or in such
CC compositions as perfumes, cosmetics, pharmaceuticals, health care
CC products, skin treatment products, pesticides, herbicides, solvents used
CC in the production of semi-conductor and integrated circuit components and
CC production materials for electronic components. The products can provide
CC for applications involving minute amounts of specific heavy metals

XX Sequence 119 AA;

Query Match 89.0%; Score 546.5; DB 2; Length 119;

Best Local Similarity 89.9%; Pred. No. 7.7e-41;

Matches 107; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVRFGTSVKVSCKASGYAFTNYLIEWVKQRPQGLEWIGVINPGSGGTNY 60

DB 1 EVQLQSGAELVRFGTSVKVSCKASGYAFTNYLIEWVKQRPQGLEWIGVINPGSGGTNY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCA-RDGP---WPFAYWGQGLTVTVSA 116

DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCA-RDGP---WPFAYWGQGLTVTVSA 119

RESULT 7

AAE34367

ID AAE34367 standard; protein; 138 AA.

XX AAE34367;

XX 14-MAY-2003 (first entry)

XX Escherichia coli heavy chain variable region.

XX S-surface antigen; Hepatitis B virus; HBV; therapy; infection; virucide;
KW hepatotropic.

XX Escherichia coli.

XX Key Location/Qualifiers

FT Region 31..35

FT Region /note= "CDR1"

FT Region 50..66

FT Region /note= "CDR2"

FT Region 99..111

FT Region /note= "CDR3"

XX W0200292819-A1.

XX 21-NOV-2002.

XX 15-MAY-2002; 2002WO-KR000905.

XX 16-MAY-2001; 2001KR-00026634.

XX (YUHA-) YUHAN CORP.

XX Lee JW, Ko IY, Kang HK, Song MY, Song TH, Kim CS;

XX WPI; 2003-140281/13.

DR N-PSDB; AAD52608.

PT New light and heavy chain variable regions of a monoclonal antibody
PT against the S-surface antigen of the hepatitis B virus (HBV), useful for
PT neutralizing or removing HBV, or for preventing or treating HBV
PT infection.
XX
XX
PS Claim 12; Page 17; 20pp; English.
XX
XX
CC The invention relates to light and heavy chain variable regions of a
CC monoclonal antibody against S-surface antigen of the hepatitis B virus
CC (HBV). The variable regions of the antibodies are useful against HBV S-
CC surface antigens, e.g. adr, adw, ayw, particularly for
CC neutralising or removing HBV. They may also be employed to treat or
CC prevent HBV infection. The present sequence is Escherichia coli heavy
CC chain variable region
XX
XX
SQ Sequence 138 AA;

Query Match 84.5%; Score 519; DB 6; Length 138;
Best Local Similarity 83.6%; Pred. No. 2.4e-38;
Matches 102; Conservative 5; Mismatches 9; Indels 6; Gaps 1;
QY 1 QVQLQSGAELVRPQTSVKVSKASGYAFTNYLIETWVKRPGQGLEWIGVINGSGGTNY 60
Db 1 QVQLQSGTEMVRPQTSVKVSKASGYFTNHLIEWVKRPGQGPPEWIGVINGSGGTNY 60
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSDSAVVFCA-----RDGPFAYWGQGLTVV 114
Db 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSDSAVVFCAIMTFLGEGYANDYWGQGSVTV 120
QY 115 SA 116
Db 121 SS 122

RESULT 8
ABG71533
ID ABG71533 standard; protein; 164 AA.
XX
XX
AC ABG71533;
XX
XX
DT 31-DEC-2002 (first entry)
XX
XX
DE Mouse anti-acetylllysine monoclonal antibody (mAb) heavy chain #1.
XX
XX
KW Mouse; anti-acetylllysine monoclonal antibody; N epsilon-acetylllysine;
KW functional analysis; acetylllysine-containing protein; pathosis;
KW acetyllated protein; disease diagnosis; histone acetylation; mAb;
KW antibody-producing immortalised cell; heavy chain.
XX
XX
OS Mus sp.
XX
XX
PN WO200274962-A1.
XX
XX
PD 26-SEP-2002.
XX
XX
PF 13-MAR-2002; 2002WO-JP002330.
XX
XX
PR 15-MAR-2001; 2001JP-00074263.
XX
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (NIHA) JAPAN ENERGY CORP.
XX
XX
PI Komatsu Y, Yoshida M;
XX
XX
DR WPI; 2002-750555/81.
DR N-PSDB; ABS55467.
XX
XX
PT Production of anti-acetylllysine monoclonal antibody capable of
PT recognizing N epsilon-acetylllysine regardless of types of adjacent
PT amino acids, useful in e.g. disease diagnosis and searching for novel
PT acetylllysine-containing proteins.
XX
XX
PS Example 4; Fig 4; 45pp; Japanese.

XX The present invention relates to a mouse anti-acetylllysine monoclonal
CC antibody (mAb) capable of recognising N epsilon-acetylllysine, and a
CC method for producing the monoclonal antibody. The produced antibody is
CC useful in searching for and functional analysis of novel acetylllysine-
CC containing proteins particularly in studying pathosis due to acetyllated
CC proteins, disease diagnosis, facilitating detection of variation in
CC acetyllation levels of histone influenced by various stimulations during
CC Western blotting, analysis of the variable region in the DNA sequence of
CC an antibody gene of an antibody-producing immortalised cell, and judging
CC the degree of homology specific to the sequence during the protein
CC translation. The monoclonal antibody of the invention is capable of
CC recognising N epsilon-acetylllysine regardless of the type of adjacent
CC amino acids and accepting adjacent amino acids over a broad range. The
CC present sequence represents a heavy chain of mouse anti-acetylllysine mAb
XX
XX
SQ Sequence 164 AA;

Query Match 84.3%; Score 517.5; DB 5; Length 164;
Best Local Similarity 84.0%; Pred. No. 4e-38;
Matches 100; Conservative 6; Mismatches 10; Indels 3; Gaps 1;
QY 1 QVQLQSGAELVRPQTSVKVSKASGYAFTNYLIETWVKRPGQGLEWIGVINGSGGTNY 60
Db 1 QVQLQSGAELVRPQTSVKVSKASGYFTNHLIEWVKRPGHGLEWIGDIYPSGTYNY 60
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSDSAVVFCA---GPFAYWGQGLTVTVA 116
Db 61 NEKFKGKATLTADTSSSTAYMQLSSLTSDSDSAIYCARSDYWGQGLTVTVA 119

RESULT 9
AAR12360
ID AAR12360 standard; protein; 137 AA.
XX
XX
AC AAR12360;
XX
XX
DT 25-MAR-2003 (revised)
DT 15-AUG-1991 (first entry)
XX
XX
DE Heavy chain variable region of murine 4D12 immunoglobulin.
XX
XX
KW Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX
XX
OS Mus musculus.
XX
XX
PN WO9107493-A.
XX
XX
PD 30-MAY-1991.
XX
XX
PF 13-NOV-1989; 89US-00433730.
XX
XX
PR 13-NOV-1989; 89US-00433730.
XX
XX
PA (XOMA) XOMA CORP.
PA (GREG) GREEN CROSS CORP.
XX
XX
PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
XX
XX
DR WPI; 1991-178105/24.
DR N-PSDB; AAQ12062.
XX
XX
PT New chimeric mouse-human antibodies - used to detect, kill and remove HIV
PT -1 antigen from sample.
XX
XX
PS Disclosure; Fig 17; 107pp; English.

XX This is the heavy - chain variable (V) region of a mouse monoclonal
CC antibody (Mab), 4D12, and is specific for an HIV-1 viral antigen. It is
CC used in the construction of a chimeric Mab comprising heavy and light
CC chains having murine V regions and human C regions. The chimeric Mabs are
CC more effective than murine Mab 4D12 since they have an increased
CC compatibility in humans. The heavy and light chain V-regions are joined

CC by manipulating their respective joining (J) regions, to generate
 CC restriction enzyme recognition sites. The chimeric MAb's can be used as
 CC immunoconjugates, in association with e.g. toxins for HIV treatment. They
 CC can also be used in diagnosis of HIV. See also AAQ12056-61 and AAQ12063.
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
 CC correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)

XX SQ Sequence 137 AA;

Query Match 83.9%; Score 515; DB 2; Length 137;
 Best Local Similarity 84.7%; Pred. No. 5.5e-38;
 Matches 100; Conservative 4; Mismatches 12; Indels 2; Gaps 1;
 QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFNTYLIIEWVKQPGGLEWIGVINPGSGGTNY 60
 DB 20 QVHLQSGAELVRPGTSVKVSKASGYAFNTYLIIEWVKQPGGLEWIGVINPGSGGTNY 79
 QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSDSAVYFCARDGPWFA--YWGQGLTVTUSA 116
 DB 80 NEKFKDKTTMTADKSSSTAYMQLSSLTSDSDSAVYLCARTGSGHALEYWGQGTSTVTSS 137

RESULT 10

AA012238
 ID AAR12238 standard; protein; 137 AA.

XX AC AAR12238;
 XX DT 25-MAR-2003 (revised)
 DT 19-AUG-1991 (first entry)
 XX DE Mouse MAb 4D12 H chain V region.
 XX KW HIV-1; chimera.

XX OS Mus sp.

XX PN WO9107494-A.

XX PD 30-MAY-1991.

XX PF 13-NOV-1989; 89US-00433703.

XX PR 13-NOV-1989; 89US-00433703.

XX PA (XOMA) XOMA CORP.

XX PA (GREG) GREEN CROSS CORP.

XX PA (ZOMA-) ZOMA CORP.

XX PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;

XX WPI: 1991-178106/24.

XX DR N-PSDB; AAQ12019.

XX CC New chimeric mouse human antibodies - used in treatment, diagnosis and
 PT prophylaxis of HIV infections.

XX PS Disclosure; Fig 17; 108pp; English.

XX CC The mouse VH gene product may be used to produce chimeric mouse- human
 CC Abs against HIV-1 comprising human Ig constant regions and murine
 CC variable regions. These novel sequence are useful in treatment, diagnosis
 CC and prophylaxis of HIV infections, and may be produced by a bacterial,
 CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 137 AA;

Query Match 83.9%; Score 515; DB 2; Length 137;
 Best Local Similarity 84.7%; Pred. No. 5.5e-38;
 Matches 100; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFNTYLIIEWVKQPGGLEWIGVINPGSGGTNY 60

DB 20 QVHLQSGAELVRPGTSVKVSKASGYAFNTYLIIEWVKQPGGLEWIGVINPGSGGTNY 79
 QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSDSAVYFCARDGPWFA--YWGQGLTVTUSA 116
 DB 80 NEKFKDKTTMTADKSSSTAYMQLSSLTSDSDSAVYLCARTGSGHALEYWGQGTSTVTSS 137

RESULT 11

AA009427

ID AAR09427 standard; protein; 141 AA.

XX AC AAR09427;

XX DT 25-MAR-2003 (revised)

DT 04-MAR-1993 (first entry)

XX DE ME4 Heavy Chain V Region (mouse).

XX KW Monoclonal antibody; chimera; light; heavy; chain; constant; variable;
 KW antigen; diagnosis; cancer; tumour.

XX OS Mus musculus.

XX PN WO9002569-A.

XX PD 22-MAR-1990.

XX PF 08-SEP-1988; 88US-00241744.

XX PR 08-SEP-1988; 88US-00241744.

XX PR 13-SEP-1988; 88US-00243739.

XX PR 04-OCT-1988; 88US-00253002.

XX PR 19-JUN-1989; 89US-00367641.

XX PR 21-JUL-1989; 89US-00382768.

XX PA (ITGE-) INT GENETIC ENG INC.

XX PA (INGE-) INGENE INT GENETIC.

XX PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;

XX WPI: 1990-115825/15.

XX DR N-PSDB; AAQ08609.

XX CC Chimeric mouse-human antibodies - prepd. using genes coding for constant
 PT human region murine variable region, esp. to 3 tumour antigen.

XX PS Claim 13; Page 123 + Fig 30; 173pp; English.

XX CC The sequence is used in the prodn. of a chimeric antibody mol. comprising
 CC two light chains and two heavy chains, each having a constant region
 CC (human) and a variable region (murine), having specificity to an antigen
 CC bound by murine monoclonal antibody (MAb) B38.1. The chimeric antibodies
 CC can be used for any purpose for which the original murine MAb's can be
 CC used, with the advantage that they are more compatible with the human
 CC body. They are esp. used for the diagnosis and treatment of cancer.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 141 AA;

Query Match 83.9%; Score 515; DB 2; Length 141;

Best Local Similarity 85.0%; Pred. No. 5.6e-38;

Matches 102; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFNTYLIIEWVKQPGGLEWIGVINPGSGGTNY 60

DB 20 QVQLQSGAELVRPGTSVKVSKCTTSGAFTNLMEMWKQRPQGLEWIGVINPGSGDAKY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSDSAVYFCARD--GPMFA--YWGQGLTVTUSA 116

DB 80 NENFKGKATLTADKSSSTAYMQLSSLTSDSDSAVYFCARGHYGGYFVMDYWGQGTSTVTUSA 139

RESULT 12

AAW06216
ID AAW06216 standard; protein; 141 AA.
XX AC AAW06216;
XX DT 25-MAR-2003 (revised)
XX DT 13-FEB-1997 (first entry)
XX DE MAB ME4 heavy chain variable region.
XX KW Chimeric antibody; monoclonal antibody; ME4; antibody engineering;
XX KW tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;
XX KW ovary carcinoma; melanoma; cancer; diagnosis; therapy; heavy chain.
XX OS Mus sp.
XX PN US5576184-A.
XX PD 19-NOV-1996.
XX PF 27-DEC-1994; 94US-00364001.
XX PR 06-SEP-1988; 88US-00240624.
XX PR 08-SEP-1988; 88US-00241744.
XX PR 13-SEP-1988; 88US-00243739.
XX PR 04-OCT-1988; 88US-00253002.
XX PR 19-JUN-1989; 89US-00367641.
XX PR 21-JUL-1989; 89US-00382768.
XX PR 06-MAY-1991; 91US-00659401.
XX PA (XOMA) XOMA CORP.
XX PI Chang CP, Lei S, Better MD, Robinson RR, Horwitz AH;
XX DR WPI; 1997-011249/01.
XX DR N-PSDB; AAT43441.
XX PT Chimeric mouse-human antibodies - recognise a human tumour antigen, used
XX PT for the treatment and diagnosis of human cancers.
XX PS Example 3; Fig 30; 102pp; English.

XX CC The heavy chain variable region (AAW06216) of mouse monoclonal antibody
CC ME4 is the product of a cDNA clone (AAT43441) isolated from a ME4
CC hybridoma cDNA library. MAB ME4 (IgG1) binds to an antigen that is
CC expressed on the surface of human lung, breast, colon and ovary
CC carcinomas and melanomas, but not on most normal adult tissues. The heavy
CC chain and light chain variable regions (see also AAW06215) of ME4 can be
CC linked to human constant regions and expressed in transformed host cells.
CC Novel mouse-human chimeric antibodies (see also AAW06209-14 and AAW06217-
CC 18) can be produced that have specificity to human tumour antigens for
CC use in the treatment and diagnosis of human cancer. (Updated on 25-MAR-
CC 2003 to correct PF field.)
XX SQ Sequence 141 AA;

Query Match 83.9%; Score 515; DB 2; Length 141;
Best Local Similarity 85.0%; Pred. No. 5.6e-38;
Matches 102; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

QY 1 QVQLQSGAEIVRPGTSVKVSKASGYAFNTYLTLEWVKORPGQGLEWIGVINGSGGTNY 60
DB 20 QVQLQSGAEIVRPGTSVKVSKCTTSVGFNTYLTLEWVKORPGQGLEWIGVINGSGDAKY 79
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD--GPWFA--YWGQGTLTVTSA 116
DB 80 NENFKGKATLTADKSSSTSYMQLSSLTSDSAVYFCARGHYGGYFYVDYWGQGTSTVTSA 139

RESULT 13

AAW85063
ID AAW85063 standard; protein; 141 AA.

XX AC AAW85063;
XX DT 20-MAR-2003 (revised)
XX DT 16-APR-1999 (first entry)
XX DE Mouse ME4 heavy chain variable region.
XX KW Heavy chain variable region; murine antibody ME4; antibody ING-1;
XX KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;
XX KW treatment; human cancer.
XX OS Mus sp.
XX PN US5843685-A.
XX PD 01-DEC-1998.
XX PF 06-JUN-1995; 95US-00466034.
XX PR 06-SEP-1988; 88US-00240624.
XX PR 08-SEP-1988; 88US-00241744.
XX PR 13-SEP-1988; 88US-00243739.
XX PR 04-OCT-1988; 88US-00253002.
XX PR 19-JUN-1989; 89US-00367641.
XX PR 21-JUL-1989; 89US-00382768.
XX PR 06-SEP-1989; 89MO-US003852.
XX PR 06-MAY-1991; 91US-00659401.
XX PR 27-DEC-1994; 94US-00364001.
XX PA (XOMA) XOMA CORP.
XX PI Horwitz AH, Lei S, Chang CP, Better MD, Robinson RR;
XX DR WPI; 1999-044574/04.
XX DR N-PSDB; AAV71159.
XX PT Chimeric antibody specific for human tumour antigen - useful as
XX PT immunoassay, imaging or antitumour agent.
XX PS Example 3; Fig 30; 92pp; English.

XX CC The present sequence represents the heavy chain variable region of murine
CC antibody ME4. The sequence was used to create chimeric mouse-human
CC immunoglobulins which recognise the human tumour antigen bound by
CC antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The
CC chimeric antibodies also have an antigen-binding site that competitively
CC inhibits the binding of antibody ING-1, and mediate complement-dependent
CC cytotoxicity of target cells or antibody-dependent cellular cytotoxicity to
CC target cells. The chimeric antibodies can be used for therapeutic
CC purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to
CC correct PR field.)
XX SQ Sequence 141 AA;

Query Match 83.9%; Score 515; DB 2; Length 141;
Best Local Similarity 85.0%; Pred. No. 5.6e-38;
Matches 102; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

QY 1 QVQLQSGAEIVRPGTSVKVSKASGYAFNTYLTLEWVKORPGQGLEWIGVINGSGGTNY 60
DB 20 QVQLQSGAEIVRPGTSVKVSKCTTSVGFNTYLTLEWVKORPGQGLEWIGVINGSGDAKY 79
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD--GPWFA--YWGQGTLTVTSA 116
DB 80 NENFKGKATLTADKSSSTSYMQLSSLTSDSAVYFCARGHYGGYFYVDYWGQGTSTVTSA 139

RESULT 14

ABU58897
ID ABU58897 standard; protein; 141 AA.
XX AC ABU58897;

XX 16-APR-2003 (first entry)

DT Mouse antibody heavy chain variable region #4.

DE Mouse; human tumour antigen; anti-human tumour antigen-antibody;

XX KW ING-1 antibody; cell line H9812; immunoassay; imaging; tumour diagnosis;

XX KW tumour therapy; cytostatic; heavy chain variable region.

OS Mus sp.

XX US6461824-B1.

XX 08-OCT-2002.

XX 06-JUN-1995; 95US-00467142.

XX 06-SEP-1988; 88US-00240624.

XX 08-SEP-1988; 88US-00241744.

PR 13-SEP-1988; 88US-00243739.

PR 04-OCT-1988; 88US-00253002.

PR 19-JUN-1989; 89US-00367641.

PR 21-JUL-1989; 89US-00382768.

PR 06-SEP-1989; 89WO-US003852.

PR 06-MAY-1991; 91US-00659401.

PR 27-DEC-1994; 94US-00364001.

XX (XOMA) XOMA TECHNOLOGY LTD.

XX Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;

PI WPI; 2003-196707/19.

XX N-PSDB; ABK79242.

XX Antibody for detecting antigen in animal or killing cells carrying

PT antigen comprises human constant region and variable region having

PT specificity for human tumor antigen bound by ING-1 antibody.

XX Example 3; Fig 30; 101pp; English.

XX The invention describes an antibody comprising a human constant region

CC and a variable region having specificity for the human tumour antigen

CC bound by the ING-1 antibody, where the ING-1 is produced by cell line

CC H9812 as deposited with ATCC, and the antibody has the same affinity as

CC the ING-1 for the human tumour antigen. The antibody is useful in an

CC immunoassay method for detecting an antigen in a sample by contacting a

CC label-detectable antigen in the sample with the antibody, detecting the

CC label and relating the detected label to the presence of the antigen; for

CC use in an imaging method for revealing the presence of a label-detectable

CC antigen in an animal by contacting the antibody with a part of the animal

CC suspected of containing the antigen, detecting the label and relating the

CC detected label to the presence of the antigen; and for killing cells

CC carrying an antigen by contacting the cells with the antibody and

CC allowing the killing to occur. The antibodies are useful in tumour

CC diagnosis and therapy. The chimeric antibodies bind to the surface of

CC human tumour cells but do not bind detectably to normal cells, e.g.,

CC fibroblasts, endothelial cells or epithelial cells in the major organs.

CC The high biological activity of the chimeric antibodies against human

CC tumour cell lines combined with minimal reactivity with normal tissues

CC imply that these antibodies may mediate selective destruction of

CC malignant tissue. The presence of human rather than murine antigenic

CC determinants on the chimeric antibodies increases their resistance to

CC rapid clearance from the body relative to the original murine mAbs. This

CC resistance to clearance enhances the potential utility of these chimeric

CC antibodies, as well as their derivatives, in tumour diagnosis and

CC therapy. This is the amino acid sequence of a mouse antibody heavy chain

CC variable region used in the creation of an anti-human tumour antigen-

CC antibody

XX Sequence 141 AA;

XX Query Match 83.9%; Score 515; DB 6; Length 141;

XX Best Local Similarity 85.0%; Pred. No. 5.6e-38;

Matches 102; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

QY 1 QVQLQQSGAELVRPGTSVKVSKASGYAFTNYLIEWKQRPQGGLEWIGVINPFGSGGTNY 60

DB 20 QVQLQQSGAELVRPGTSVKVSKTTSYGAFNYLMEWMKQRPQGGLEWIGVINPFGSGDAKY 79

QY 61 NEKFKGKATLTADKSSSTAYNQLSSLTSDSAYVFCARD--GPWFA--YWGQGLTVTVSA 116

DB 80 NENFKGKATLTADKSSSTSYNQLSSLTSDSAYVFCARGHYGGYFVNDYWGQGLTVTVSA 139

RESULT 15

AAW34515

ID AAW34515 standard; protein; 138 AA.

XX AC AAW34515;

XX 19-MAR-1998 (first entry)

DT Variable heavy chain of antibody from hybridoma 5-465-210.

DE Variable region coding sequence; constant region epitope; hybridoma;

XX KW antibody detection; antigen/antibody complex; variable heavy chain.

XX OS Mus musculus.

XX WO9727486-A1.

XX 31-JUL-1997.

XX 17-JAN-1997; 97WO-US001074.

XX 23-JAN-1996; 96US-00589939.

XX (ABBO) ABBOTT LAB.

XX Hackett JR, Hoff JA, Ostrow DH, Golden AM;

XX WPI: 1997-393833/36.

XX N-PSDB; AAT98832.

XX Use of antibody constant region epitope(s) - as control or calibrator

PT reagents in assays for detecting the presence of an antibody in a test

PT sample.

XX Disclosure; Page 60; 109pp; English.

XX This sequence represents the variable heavy chain of the antibody

CC produced by hybridoma 5-465-210, and can be detected using the method of

CC the invention. The method is for detecting the presence of antibody which

CC may be present in a test sample. It comprises contacting a test sample

CC suspected of containing the antibody with an antigen specific for the

CC antibody to allow the formation of antigen/antibody complexes, detecting

CC the presence of the antibody which may be present in the test sample and

CC employing, as a control or calibrator, a reagent which binds to the

CC antigen. The improvement to this method over previous methods, comprises

CC employing, as the control or calibrator, a reagent comprising one or more

CC antibody constant region epitopes, where the reagent binds to the antigen

CC and is homogeneous with respect to specificity and affinity. The method

CC can be also be used for detecting the presence of antibodies developed

CC against more than one antigen. The method is used particularly for the

CC detection of human antibodies specific for a given antigen, e.g. HIV-1,

CC hepatitis B virus, rubella virus, etc. Use of the reagents circumvent all

CC of the problems associated with using an immune sera in the manufacture

CC of calibrators and positive controls. The present reagents can be readily

CC and reproducibly generated in virtually unlimited quantities and are also

CC useful for quantitating, and monitoring the integrity of, the antigen

CC used in assays

XX Sequence 138 AA;

XX Query Match 83.1%; Score 510.5; DB 2; Length 138;

XX Best Local Similarity 84.9%; Pred. No. 1.4e-37;

Matches 101; Conservative 5; Mismatches 10; Indels 3; Gaps 1;
QY 1 QVQLQQSGAELVREGTSVKYSCKASGYFTNLYIEWKQRPQGQLEWIGVINPGSGTNY 60
DQ 20 QVHLQQSGAELVREGTSVKYSCKASGYFTNLYIEWTQRPQGQLEWIGVINPGSDFTYY 79
QY 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAYVFCAR---DGPWFAYWGQGLVTVSA 116
DQ 80 NEKFKGRATLTADKSSSTAYMQLSLTSDSAYVFCARTIVTTDYPDWGQGLPLTVSS 138

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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-889-300A-2
Perfect score: 562
Sequence: 1 NIVMTQPKMSMSVGRVT.....CGQSYVPYTFGGTKLEIK 107

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Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

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Post-processing: Minimum Match 0%
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Database : A_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
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4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	562	100.0	107	2	AAW47086
2	562	100.0	107	2	AAW47086
3	562	100.0	107	2	AAW47086
4	562	100.0	107	3	AAW47086
5	562	100.0	109	2	AAW47086
6	562	100.0	121	2	AAW47086
7	562	100.0	121	2	AAW47086
8	562	100.0	121	2	AAW47086
9	562	100.0	127	2	AAW47086
10	562	100.0	132	6	AAW47086
11	562	100.0	135	7	AAW47086
12	562	100.0	135	7	AAW47086
13	534	95.0	101	5	AAW47086
14	527	93.8	136	2	AAW47086
15	521	92.7	127	3	AAW47086
16	521	92.7	136	4	AAW47086
17	509	90.6	108	2	AAW47086
18	503	89.5	107	6	AAW47086
19	503	89.5	107	6	AAW47086
20	503	89.5	107	6	AAW47086
21	490	87.2	107	6	AAW47086
22	490	87.2	107	6	AAW47086
23	490	87.2	107	6	AAW47086
24	490	87.2	107	6	AAW47086
25	490	87.2	107	6	AAW47086

26	490	87.2	107	6	ABR44681	AbR44681 Murine J4
27	487	86.7	107	6	ABO10739	AbO10739 Variable
28	487	86.7	107	6	ABR44625	AbR44625 Murine J4
29	487	86.7	107	6	ABR44683	AbR44683 Murine J4
30	485	86.3	107	6	ABO10736	AbO10736 Variable
31	485	86.3	107	6	ABR44680	AbR44680 Murine J4
32	485	86.3	107	6	ABR44621	AbR44621 Murine J4
33	484	86.1	107	6	ABO10741	AbO10741 Consensus
34	484	86.1	107	6	ABO10729	AbO10729 Variable
35	484	86.1	107	6	ABO10740	AbO10740 Variable
36	484	86.1	107	6	ABR44684	AbR44684 Murine J4
37	484	86.1	107	6	ABR44623	AbR44623 Murine J4
38	484	86.1	107	6	ABR44625	AbR44625 Murine J4
39	484	86.1	107	6	ABR44685	AbR44685 Murine J4
40	484	86.1	107	6	ABR44617	AbR44617 Murine J4
41	484	86.1	107	6	ABR44673	AbR44673 Murine J4
42	482	85.8	239	2	AAW46812	AAW46812 SCFv anti
43	478	85.1	107	6	ABO10735	AbO10735 Variable
44	478	85.1	107	6	ABR44620	AbR44620 Murine J4
45	478	85.1	107	6	ABR44679	AbR44679 Murine J4

ALIGNMENTS

RESULT 1
AAW47086
ID AAW47086 standard; protein; 107 AA.
XX
AC AAW47086;
XX
DT 26-JUN-1998 (first entry)
XX
DE Mouse J591 monoclonal antibody light chain variable region.
XX
KW Mouse; monoclonal antibody; J591; prostate specific membrane antigen;
KW cancer; vascular endothelial cell; metastatic adenocarcinoma.
XX
OS Mus sp.
XX
FN WO9803973-A1.
XX
PD 29-JAN-1998.
XX
PF 17-JUL-1997; 97WO-US012035.
XX
PR 18-JUL-1996; 96US-0022125P.
PR 09-APR-1997; 97US-00838682.
(CORR) CORNELL RES FOUND INC.
Bander NH;
WPI; 1998-120937/11.
N-PSDB; AAV13952.
Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or on normal, hypertrophic or cancerous prostatic cells, also used for diagnosis.
Example 12; Page 60; 94pp; English.
The present sequence represents the mouse J591 monoclonal antibody light chain variable region from an example of the present invention. The present invention describes the elimination of cancer cells by treating vascular endothelial cells (VEC) close to the cancer with an agent (A) able to bind to the extracellular domain (ECD) of prostate specific membrane antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells. Also described are: (1) the detection of cancer tissue by detecting binding of labelled (A) to VEC close to, or within, a cancer tissue; (2) eliminating or detecting normal, benignly hyperplastic or cancerous prostate epithelial cells using optionally labelled (A); (3)

CC hybridomas that produce a monoclonal antibody (MAb) that binds to PSMA.
 CC The method is used to treat renal, urothelial, colon, lung, rectal or
 CC breast cancers and metastatic adenocarcinoma of the liver. The diagnostic
 CC method is particularly used to detect recurrence of prostatic disease or
 CC to monitor the effect of treatments for prostate cancer (presence of PSMA
 CC in the serum indicates that prostate cells are being lysed). (A) binds to
 CC an epitope of PSMA expressed on live cells (contrast antibody 7E11 which
 CC only binds after cell lysis), allowing targeting of live, unfixed cells
 CC and thus providing more efficient treatment and diagnosis. Both cancer
 CC cells themselves and the VEC on which they depend are killed. All VEC
 CC close to cancer cells express PSMA, whatever the type of cancer, but
 CC normal VEC do not
 XX
 XX

SQ Sequence 107 AA;

Query Match 100.0%; Score 562; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.1e-39;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIWMTQSPKSMVSGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60
 DB 1 NIWMTQSPKSMVSGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60
 QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTKEIK 107
 DB 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTKEIK 107

RESULT 2

AAV90374
 ID AAV90374 standard; protein; 107 AA.

XX AAY90374;

XX 15-JAN-2001 (first entry)

XX J591 monoclonal antibody light chain protein sequence fragment.

XX J591 monoclonal antibody; extracellular domain; diagnosis; therapy;
 XX prostate specific membrane antigen; prostate cancer; light chain.

XX Homo sapiens.

XX US6107090-A.

XX 22-AUG-2000.

XX 09-APR-1997; 97US-00838682.

XX 06-MAY-1996; 96US-0016976P.

XX 18-JUL-1996; 96US-0022125P.

XX (CORR) CORNELL RES FOUND INC.

XX Bander NH;

XX WPI; 1998-120937/11.

XX N-PSDB; AAA37834.

XX Destroying cancer cells with agent that binds to prostate specific
 XX membrane antigen - on vascular endothelial cells near the cancer, or on
 XX normal, hypertrophic or cancerous prostatic cells, also used for
 XX diagnosis.

XX Example 12; Col 22; 33pp; English.

XX This sequence is a fragment of the light chain of the monoclonal antibody
 XX J591. The invention relates to an isolated antibody or its antigen
 XX binding portion (I) which binds to an extracellular domain of prostate
 XX specific membrane antigen and which does not require cell lysis to bind
 XX to the extracellular domain. The antibody or its antigen binding portion
 XX is selected for its ability to bind to live cells. (I) is useful for
 XX diagnosis of diseases associated with the presence of normal, benign

CC hyperplastic, and cancerous epithelial cells or portions. Also it can be
 CC used for identifying the recurrence of such diseases, particularly when
 CC the disease is localised in a particular biological material of the
 CC patient for e.g. recurrence of prostatic disease. They can also be used
 CC alone or bound to a substance effective to kill cancerous prostate
 CC epithelial cells as a therapy for prostate cancer. Binding and
 CC internalising of the antibody with the prostate specific membrane
 CC antigen, permits the therapeutic use of intracellularly acting cytotoxic
 CC agents. (I) targets only prostate epithelial cells and other tissue are
 CC spared which provides safer treatment particularly for elderly patients.
 CC The antibodies bind to living prostate cells and treatments using these
 CC antibodies are more effective than those which target lysed prostate
 CC cells
 XX
 XX

SQ Sequence 107 AA;

Query Match 100.0%; Score 562; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.1e-39;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIWMTQSPKSMVSGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60
 DB 1 NIWMTQSPKSMVSGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60

QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTKEIK 107

DB 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTKEIK 107

RESULT 3

AAAB36225

ID AAB36225 standard; protein; 107 AA.

XX AAB36225;

XX 15-FEB-2001 (first entry)

XX Monoclonal antibody J591 kappa light chain V region #1.

XX Mouse; antibody; heavy chain; prostate cancer; biological agent.

XX Mus sp.

XX US6136311-A.

XX 24-OCT-2000.

XX 17-JUL-1997; 97US-00895914.

XX 06-MAY-1996; 96US-0016976P.

XX 18-JUL-1996; 96US-0022125P.

XX 09-APR-1997; 97US-00838682.

XX (CORR) CORNELL RES FOUND INC.

XX Bander NH;

XX WPI; 1998-120937/11.

XX N-PSDB; AAC66544.

XX Destroying cancer cells with agent that binds to prostate specific
 XX membrane antigen - on vascular endothelial cells near the cancer, or on
 XX normal, hypertrophic or cancerous prostatic cells, also used for
 XX diagnosis.

XX Example 12; Col 25; 35pp; English.

XX The present invention describes a method of killing cancer cells,
 XX particularly prostate cancer cells, by directing a biological agent to
 XX the cells which then binds to a prostate specific membrane antigen and
 XX causes the molecule to be internalised. The internalisation of the agent,
 XX which may be bound to a drug or which may act to kill the cell alone,
 XX then leads to the death of the cell. The present sequence forms part of

CC an antibody which may be used as the biological agent of the invention.
CC In addition to prostate cancer, the method can be used with renal,
CC urothelial, colon, renal, lung and breast cancer cells, and cancerous
CC cells of metastatic adenocarcinoma to the liver
XX Sequence 107 AA;
SQ
Query Match 100.0%; Score 562; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIVMTQSPKSMVSGRVTITCKASENVVTVYSWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 1 NIVMTQSPKSMVSGRVTITCKASENVVTVYSWYQKPEQSPKLLIYGASNRYTGVPD 60
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGSYPYTFGGGTGLEIK 107
Db 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGSYPYTFGGGTGLEIK 107
RESULT 4
AAB10444
ID AAB10444 standard; protein; 107 AA.
AC AAB10444;
XX
XX 01-DEC-2000 (first entry)
DT Murine monoclonal antibody MAK HE2 variable region light chain.
DE Murine monoclonal antibody; MAK HE2; light chain; variable region;
KW human cellular membrane antigen; tumor associated antigen; TAA; vaccine;
KW cancer.
XX
XX Mus sp.
OS
XX WO200041722-A1.
FN
XX 20-JUL-2000.
PD
XX 12-JAN-2000; 2000WO-EP000174.
PF
XX 13-JAN-1999; 99CH-000000051.
PR
XX (IGEN-) IGENEON GMBH.
PA
XX Eckert H, Leibner H;
PI
XX WPI; 2000-475956/41.
DR
XX Novel use of antibodies against human cellular membrane antigens for
PT vaccination against cancer.
PT
XX Example 3; Page 47-48; 54pp; German.
PS
XX This invention describes the novel use of an antibody targeted to a human
CC cellular membrane antigen, to manufacture a medicament to
CC prophylactically and/or therapeutically vaccinate against cancer. The
CC antibodies against tumor associated antigen (TAA) for prophylactic and/or
CC therapeutic vaccination against cancer may be used in low doses (when
CC compared to antibodies against TAA for passive immunotherapy), typically
CC less than 1 mg by injection. The antibodies also have a long continual
CC activity that directly induces immunity and their shelf life is unlimited
CC (fresh vaccination is always possible). This sequence represents the
CC murine monoclonal antibody MAK HE2 variable region light chain fragment
CC which is used in the method of the invention
XX
XX Sequence 107 AA;
SQ
Query Match 100.0%; Score 562; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIVMTQSPKSMVSGRVTITCKASENVVTVYSWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 1 NIVMTQSPKSMVSGRVTITCKASENVVTVYSWYQKPEQSPKLLIYGASNRYTGVPD 60
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGSYPYTFGGGTGLEIK 107
Db 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGSYPYTFGGGTGLEIK 107
RESULT 5
AAR27144
ID AAR27144 standard; protein; 109 AA.
AC AAR27144;
XX
XX 25-MAR-2003 (revised)
DT 20-MAY-1998 (first entry)
DT
XX 1E6 kappa light chain variable region.
DE
XX Chimeric; heavy chain; variable region; monoclonal antibody;
KW lymphocyte function associated antigen-3; LFA-3; inflammation;
KW autoimmune disease; immunomodulation; systemic lupus erythematosus;
KW rheumatoid arthritis; thyroiditis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH domain 24..34
FT domain /note= "CDR1"
FT domain 50..56
FT domain /note= "CDR2"
FT domain 89..97
FT domain /note= "CDR3"
XX
XX EP03646-A1.
PN
XX 16-SEP-1992.
PD
XX 12-MAR-1992; 92EP-00104318.
PF
XX 12-MAR-1991; 91US-00667975.
PR
XX (BIOJ) BIOGEN INC.
PA
XX Sato VL, Chisholm PL, Wallner BP;
PI
XX WPI; 1992-309758/38.
DR
XX N-PSDB; AAQ28653.
DR
XX Monoclonal antibodies active against lymphocyte function associated
PT antigen-3 - for treating inflammation and autoimmune diseases, and for
PT detecting LFA-3 protein in a sample.
PT
XX Claim 19; Page 14; 30pp; English.
PS
XX Light and heavy chain variable region sequences were deduced from the DNA
CC sequences obd. by PCR of DNA sequences obd. from the hybridoma cell
CC line 1E6-2C12 (ATCC HB 10693). The light and heavy chain regions may be
CC used to construct a monoclonal antibody active against LFA-3 which blocks
CC adhesion of LFA-3 expressing cells to lymphocytes. The antibody may be
CC used in the treatment and diagnosis of acute and chronic inflammation,
CC autoimmune diseases and for immuno- modulation including systemic lupus
CC erythematosus, rheumatoid arthritis and thyroiditis. See also AAR27145.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 109 AA;
SQ
Query Match 100.0%; Score 562; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.2e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIVMTQSPKSMVSGRVTITCKASENVVTVYSWYQKPEQSPKLLIYGASNRYTGVPD 60

```
Db 1 NIVMTQSPKSMVSGERVTLTCKASENVVTVYSWYQOKPEQSPKLLIYGASNRYTGVPD 60
Qy 61 RFTGSGSATDFTLTISVQAEDLADYHCQGQYSYPYTFGGGTGLEIK 107
Db 61 RFTGSGSATDFTLTISVQAEDLADYHCQGQYSYPYTFGGGTGLEIK 107

RESULT 6
AAW47085
ID AAW47085 standard; protein; 121 AA.
XX
AC AAW47085;
XX
DT 26-JUN-1998 (first entry)
XX
XX Mouse J591 monoclonal antibody light chain.
XX
DE Mouse; monoclonal antibody; J591; prostate specific membrane antigen;
XX cancer; vascular endothelial cell; metastatic adenocarcinoma.
XX
XX Mus sp.
XX
XX WO9803873-A1.
XX
XX 29-JAN-1998.
XX
XX 17-JUL-1997; 97WO-US012035.
XX
XX 18-JUL-1996; 96US-0022125P.
XX
XX 09-APR-1997; 97US-00838682.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Bander NH;
XX
XX WPI; 1998-120937/11.
XX
XX N-PSDB; AAV13951.
XX
XX Destroying cancer cells with agent that binds to prostate specific
XX membrane antigen - on vascular endothelial cells near the cancer, or on
XX normal, hypertrophic or cancerous prostatic cells, also used for
XX diagnosis.
XX
XX Example 12; Page 57; 94pp; English.
XX
XX The present sequence represents the mouse J591 monoclonal antibody light
XX chain from an example of the present invention. The present invention
XX describes the elimination of cancer cells by treating vascular
XX endothelial cells (VEC) close to the cancer with an agent (A) able to
XX bind to the extracellular domain (ECD) of prostate specific membrane
XX antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells.
XX Also described are: (1) the detection of cancer tissue by detecting
XX binding of labelled (A) to VEC close to, or within, a cancer tissue; (2)
XX eliminating or detecting normal, benignly hyperplastic or cancerous
XX prostate epithelial cells using optionally labelled (A); (3) hybridomas
XX that produce a monoclonal antibody (MAB) that binds to PSMA. The method
XX is used to treat renal, urothelial, colon, lung, rectal or breast cancers
XX and metastatic adenocarcinoma of the liver. The diagnostic method is
XX particularly used to detect recurrence of prostatic disease or to monitor
XX the effect of treatments for prostate cancer (presence of PSMA in the
XX serum indicates that prostate cells are being lysed). (A) binds to an
XX epitope of PSMA expressed on live cells (contrast antibody 7E11 which
XX only binds after cell lysis), allowing targeting of live, unfixed cells
XX and thus providing more efficient treatment and diagnosis. Both cancer
XX cells themselves and the VEC on which they depend are killed. All VEC
XX close to cancer cells express PSMA, whatever the type of cancer, but
XX normal VEC do not
XX
XX Sequence 121 AA;
```

Query Match 100.0%; Score 562; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. NO. 4.7e-39;

```
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NIVMTQSPKSMVSGERVTLTCKASENVVTVYSWYQOKPEQSPKLLIYGASNRYTGVPD 60
Db 7 NIVMTQSPKSMVSGERVTLTCKASENVVTVYSWYQOKPEQSPKLLIYGASNRYTGVPD 66
Qy 61 RFTGSGSATDFTLTISVQAEDLADYHCQGQYSYPYTFGGGTGLEIK 107
Db 67 RFTGSGSATDFTLTISVQAEDLADYHCQGQYSYPYTFGGGTGLEIK 113

RESULT 7
AAY90370
ID AAY90370 standard; protein; 121 AA.
XX
AC AAY90370;
XX
DT 15-JAN-2001 (first entry)
XX
XX J591 monoclonal antibody kappa light chain protein sequence #1.
XX
DE J591 monoclonal antibody; extracellular domain; diagnosis; therapy;
XX prostate specific membrane antigen; prostate cancer; kappa light chain.
XX
XX Homo sapiens.
XX
XX US6107090-A.
XX
XX 22-AUG-2000.
XX
XX 09-APR-1997; 97US-00838682.
XX
XX 06-MAY-1996; 96US-0016976P.
XX
XX 18-JUL-1996; 96US-0022125P.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Bander NH;
XX
XX WPI; 1998-120937/11.
XX
XX N-PSDB; AAA37832.
XX
XX Destroying cancer cells with agent that binds to prostate specific
XX membrane antigen - on vascular endothelial cells near the cancer, or on
XX normal, hypertrophic or cancerous prostatic cells, also used for
XX diagnosis.
XX
XX Example 12; Fig 10; 33pp; English.
XX
XX This sequence is the kappa light chain of the monoclonal antibody J591.
XX The invention relates to an isolated antibody or its antigen binding
XX portion (I) which binds to an extracellular domain of prostate specific
XX membrane antigen and which does not require cell lysis to bind to the
XX extracellular domain. The antibody or its antigen binding portion is
XX selected for its ability to bind to live cells. (I) is useful for
XX diagnosis of diseases associated with the presence of normal, benign
XX hyperplastic, and cancerous epithelial cells or portions. Also it can be
XX used for identifying the recurrence of such diseases, particularly when
XX the disease is localised in a particular biological material of the
XX patient for e.g. recurrence of prostatic disease. They can also be used
XX alone or bound to a substance effective to kill cancerous prostate
XX epithelial cells as a therapy for prostate cancer. Binding and
XX internalising of the antibody with the prostate specific membrane
XX antigen, permits the therapeutic use of intracellularly acting cytotoxic
XX agents. (I) targets only prostate epithelial cells and other tissue are
XX spared which provides safer treatment particularly for elderly patients.
XX The antibodies bind to living prostate cells and treatments using these
XX antibodies are more effective than those which target lysed prostate
XX cells
XX
XX Sequence 121 AA;
```

Query Match 100.0%; Score 562; DB 2; Length 121;

Best Local Similarity 100.0%; Pred. No. 4.7e-39; Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMMSGVGRVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 7 NIVMTQSPKSMMSGVGRVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 66

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIK 107
Db 67 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIK 113

RESULT 8
AAB36222
ID AAB36222 standard; protein; 121 AA.
AC AAB36222;
XX
DT 15-FEB-2001 (first entry)
XX
DE Murine monoclonal antibody J591 kappa light chain #1.
XX
KW Mouse; antibody; heavy chain; prostate cancer; biological agent.
XX
OS Mus sp.
XX
PN US6136311-A.
XX
PD 24-OCT-2000.
XX
PF 17-JUL-1997; 97US-00895914.
XX
PR 06-MAY-1996; 96US-0046976P.
PR 18-JUL-1996; 96US-0022125P.
PR 09-APR-1997; 97US-00838682.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Bander NH;
XX
DR WPI; 1998-120937/11.
DR N-PSDB; AAC66542.
XX
PT Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or on normal, hypertrophic or cancerous prostatic cells, also used for diagnosis.
XX
PS Example 12; Fig 10; 35pp; English.
XX
CC The present invention describes a method of killing cancer cells, particularly prostate cancer cells, by directing a biological agent to the cells which then binds to a prostate specific membrane antigen and causes the molecule to be internalised. The internalisation of the agent, which may be bound to a drug or which may act to kill the cell alone, then leads to the death of the cell. The present sequence forms part of an antibody which may be used as the biological agent of the invention. CC In addition to prostate cancer, the method can be used with renal, urothelial, colon, renal, lung and breast cancer cells, and cancerous cells of metastatic adenocarcinoma to the liver
XX
SQ Sequence 121 AA;

Query Match 100.0%; Score 562; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.7e-39; Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMMSGVGRVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 7 NIVMTQSPKSMMSGVGRVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 66

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIK 107

Db 67 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIK 113

RESULT 9
AAW01145
ID AAW01145 standard; protein; 127 AA.
XX
AC AAW01145;
XX
DT 10-FEB-1997 (first entry)
XX
DE MAb 10.1 light chain, directed against type II phospholipase A2.
XX
KW Monoclonal antibody; phospholipase; myocardial infarction; pancreatitis; cerebral infarction; acute kidney failure; colitis; chronic rheumatism; adult respiratory distress syndrome; cardiac shock; treatment; preclinical testing; disease; hybridoma.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Binding-site 44..54
FT Binding-site /label= CDR 1
FT Binding-site 70..76
FT Binding-site /label= CDR 2
FT Binding-site 109..117
FT Binding-site /label= CDR 3
XX
PN WO9620959-A1.
XX
PD 11-JUL-1996.
XX
PF 27-DEC-1995; 95WO-JP002714.
XX
PR 29-DEC-1994; 94JP-00340006.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PI Kawauchi Y, Takasaki J, Yasunaga T, Masuho Y;
XX
DR WPI; 1996-333946/33.
DR N-PSDB; AAT40805.
XX
PT Monoclonal antibody inhibiting type II phospholipase A2 activity - for treatment of myocardial and cerebral infarction.
XX
PS Claim 6; Fig 13; 69pp; Japanese.
XX
CC Monoclonal antibodies which inhibit type II phospholipase A2 are useful in the treatment of myocardial infarction, cerebral infarction, acute kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult respiratory distress syndrome and colitis. The antibodies were generated by immunising Balb/C mice with recombinant human type II phospholipase A2. Spleen cells from the mice were fused with mouse myeloma P3U1 (P3x63Ag8.U1) and the hybridomas obtained were screened for phospholipase A2 inhibitory activity. Active clones were isolated including 12H5, 1.4 and 10.1. These were cultured and the antibody isolated from the culture supernatant by precipitation with ammonium sulphate and purification on a column of protein A-Sepharose CL4B. Because the antibody acts on the primate and mouse forms of enzyme as well as human it is particularly suitable for preclinical testing
XX
SQ Sequence 127 AA;

Query Match 100.0%; Score 562; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 4.9e-39; Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMMSGVGRVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 21 NIVMTQSPKSMMSGVGRVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 80

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIK 107

XX Hybridoma HB22-196 anti-CD22 Mab kappa light chain V-J junction.
 XX
 XX CD22; autoimmune disease; anti-CD22 antibody; immunosuppressive;
 KW cytostatic; nephrotropic; dermatological; anti-inflammatory; anti-ulcer;
 KW antirheumatic; antiarthritic; antiposoriatic; thyromimetic; antianemic;
 KW antidiabetic; antiallergic; gene therapy; HB22-196.
 XX
 OS Homo sapiens.
 XX
 XX WO2003072736-A2.
 XX
 XX PD 04-SEP-2003.
 XX
 XX PF 21-FEB-2003; 2003WO-US005549.
 XX
 PR 21-FEB-2002; 2002US-0358419P.
 PR 21-OCT-2002; 2002US-0420472P.
 XX
 XX (UYDU-) UNIV DUKE.
 XX
 XX Tedder TF;
 XX
 XX WPI; 2003-721765/68.
 DR N-PSDB; ACF36501.
 XX
 XX Treating an autoimmune disease or a B-cell malignancy in a human patient
 PT comprises administering an amount of an anti-CD22 monoclonal antibody to
 PT the patient and monitoring the response of the disease to the treatment.
 XX
 XX Claim 4; Fig 23; 69pp; English.
 XX
 XX The invention relates to treating a human patient diagnosed with an
 CC autoimmune disease. The method involves administering to the patient an
 CC amount of a blocking anti-CD22 monoclonal antibody and monitoring the
 CC response of the autoimmune disease to the treatment. The method is useful
 CC in treating autoimmune diseases (e.g. glomerulonephritis, systemic lupus
 CC erythematosus, rheumatoid arthritis, psoriasis, ulcerative colitis,
 CC Hashimoto's thyroiditis, autoimmune haemolytic anemias, diabetes or
 CC allergies) or B-cell malignancies (e.g. lymphomas or leukemias). The
 CC present sequence represents the amino acid sequence for kappa light chain
 CC V-J junction for anti-CD22 antibody from hybridoma HB22-196
 XX
 XX Sequence 135 AA;
 SQ
 Query Match 100.0%; Score 562; DB 7; Length 135;
 Best Local Similarity 100.0%; Pred. No. 5.2e-39;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NIVMTQSPKMSMSVGERVLTCKASENVVTVSVYQQRPEQSPKLLIYGASNRVTGVPD 60
 DB 21 NIVMTQSPKMSMSVGERVLTCKASENVVTVSVYQQRPEQSPKLLIYGASNRVTGVPD 80
 QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPVTFGGTKLEIK 107
 DB 81 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPVTFGGTKLEIK 127
 RESULT 13
 ABB07176
 ID ABB07176 standard; protein; 101 AA.
 XX
 XX ABB07176;
 XX
 XX 13-MAR-2002 (first entry)
 DT Mouse 09 antibody kappa light chain 1 variable region.
 DE
 XX Neuromodulatory; central nervous system; CNS; sHGM22; LYM 22; AKJR4;
 KW ebvHGM Msl19D10; ebv HGM CB2bG8; CB2IE12; MS119E5; virucide;
 KW antiparkinsonian; neuroprotective; nootropic; vulnerary; mouse.
 XX
 OS Mus sp.

XX WO200185797-A1.
 XX
 XX 15-NOV-2001.
 XX
 XX 30-MAY-2000; 2000WO-US014902.
 XX
 XX 10-MAY-2000; 2000US-00568351.
 XX
 XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
 XX
 XX Rodriguez M, Miller DJ, Pease LR;
 XX
 XX WPI; 2002-066596/09.
 DR N-PSDB; ABA94223.
 XX
 XX Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
 PT neurite outgrowth, regeneration, remyelination and neuroprotection in
 PT central nervous system, useful to treat post-infectious
 PT encephalomyelitis.
 XX
 XX Disclosure; Fig 35A-B; 219pp; English.
 XX
 XX The invention provides a neuromodulatory agent (I) capable of promoting
 CC neurite outgrowth, regeneration, remyelination and neuroprotection in
 CC central nervous system (CNS). (I) is capable of inducing remyelination,
 CC promoting cellular proliferation of glial cells, and promoting Ca2+
 CC signaling with oligodendrocytes. An humanised antibody to (I) can be
 CC selected from antibody sHGM22 (LYM 22), ebvHGM Msl19D10, ebv HGM
 CC CB2bG8, AKJR4, CB2IE12, CB2IE7 or MS119E5. (I) is useful for stimulating
 CC remyelination of CNS axons, stimulating proliferation of glial cells in
 CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
 CC of such therapy. (I) is capable of binding to structures and cells within
 CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
 CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
 CC (TMEV) or for treating a human being having multiple sclerosis, or a
 CC human or domestic animal with a viral demyelinating disease, or a post-
 CC neural disease of CNS. (I) is also useful for an in vitro method of
 CC stimulating the proliferation of glial cells from mixed cell culture. (I)
 CC is also useful for stimulating remyelination of CNS axons. The antibodies
 CC are useful for preventing infection by a bacterium, virus or like
 CC pathogen that causes demyelination or other neurodegenerative condition
 CC in a subject. Methods where (I) is administered to a patient are useful
 CC for treating multiple sclerosis, Parkinson's disease, Alzheimer's
 CC disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
 CC disease, CNS diseases, and other conditions in the CNS where nerves are
 CC damaged as by trauma. The present sequence represents the mouse 09
 CC antibody kappa light chain 1 variable region
 XX
 XX Sequence 101 AA;
 SQ
 Query Match 95.0%; Score 534; DB 5; Length 101;
 Best Local Similarity 100.0%; Pred. No. 8e-37;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NIVMTQSPKMSMSVGERVLTCKASENVVTVSVYQQRPEQSPKLLIYGASNRVTGVPD 60
 DB 1 NIVMTQSPKMSMSVGERVLTCKASENVVTVSVYQQRPEQSPKLLIYGASNRVTGVPD 60
 QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPVTFGG 101
 DB 61 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPVTFGG 101
 RESULT 14
 AAW01632
 ID AAW01632 standard; protein; 136 AA.
 XX
 XX AAW01632;
 XX
 XX 22-JUL-1997 (first entry)
 DT Ber-H2 heavy kappa chain.

```

XX CD30; immunoglobulin; variable region; CDR; cancer; diagnosis; therapy;
KW Ber-H2.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..29
XX Protein /label= sig_peptide
XX 30..136
XX /label= mat_protein
XX
XX DE19543039-C1.
XX
XX 21-NOV-1996.
XX
XX 08-NOV-1995; 95DE-01043039.
XX
XX 08-NOV-1995; 95DE-01043039.
XX (MEDA-) MEDAC GES KLINISCHE SPEZIALPRAEPARATE.
XX
XX Ziegler A, Stein H;
XX
XX WPI; 1996-507017/51.
XX N-PSDB; AAT58329.
XX
XX DNA mols. encoding CD30-specific immunoglobulin variable regions - useful
XX for cancer diagnosis or therapy.
XX
XX Claim 15; Page 15; 20pp; German.
XX
XX The ligands are useful for diagnosis or therapy of CD30 expressing
XX cancers, esp. Hodgkinson's disease. Cytoplasmic RNA was isolated from
XX cells of the mouse myeloma hybrid line Ber-H2. cDNA was isolated using
XX reverse transcriptase. A VHDJ fragment cont. band was cut from a gel and
XX purified. DNA corresponding to VK and Vgamma was isolated and cloned into
XX vectors. Oligonucleotides used are given in AAT58331 to AAT58340
XX
XX Sequence 136 AA;
XX
XX Query Match 93.8%; Score 527; DB 2; Length 136;
XX Best Local Similarity 94.4%; Pred. No. 4, 1e-36;
XX Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 NIVMTQSPKMSMSVGERVTLTKASENVTVVSWYQKPSQPKLLIYGASNRYTGVPD 60
XX 30 NIVMTQSPKMSMSVGERVTLTKASENVTVVSWYQKPSQPKLLIYGASNRYTGVPD 89
XX
XX 61 RFTGSGSATDFTLTISVQAEADLYHCGQGYSPYPTFGGKLEIK 107
XX 90 RFTGSGSATDFTLTISVQAEADLYHCGQGYSPYPTFGGKLEIK 136
XX
XX RESULT 15
XX AAY71545
XX ID AAY71545 standard; protein; 127 AA.
XX
XX AC AAY71545;
XX
XX 12-OCT-2000 (first entry)
XX
XX Mouse AF2 antibody light chain variable region (AF2-VL).
XX
XX Humanised antibody; HuZAF; mouse AF2 antibody; human EU antibody; AF2-VL;
XX light chain variable region; VL; heavy chain variable region; VH; IgG2b;
XX gamma-interferon; IFN; complementarity determining region; CDR; FR;
XX framework region; immunosuppressive; antiinflammatory; antisclerotic;
XX gastrointestinal; antidiabetic; antiarthritic; dermatological; inhibitor;
XX autoimmune disease; graft versus host disease; organ transplant;
XX multiple sclerosis; Type I diabetes; rheumatoid arthritis; psoriasis;
XX systemic lupus erythematosus; SLE; Crohn's disease.
XX

```

```

OS Mus sp.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX Protein /note= "N-terminal peptide"
XX 21..127
XX /note= "Mature mouse antibody AF2 light chain variable
XX region (AF2-VL)"
XX 44..54
XX /label= CDR
XX /note= "Complementarity determining region"
XX 70..76
XX /label= CDR
XX /note= "Complementarity determining region"
XX 109..117
XX /label= CDR
XX /note= "Complementarity determining region"
XX
XX WO20032634-A1.
XX
XX 08-JUN-2000.
XX
XX 29-NOV-1999; 99WO-US028195.
XX
XX 01-DEC-1998; 98US-0110523P.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Vasquez M, Landolfi NF, Tsurushita N, Queen CL;
XX
XX WPI; 2000-412292/35.
XX N-PSDB; AAD01345.
XX
XX Humanized murine AF2 immunoglobulins, useful for inhibiting gamma-
XX interferon for the treatment of autoimmune diseases, e.g. multiple
XX sclerosis and diabetes.
XX
XX Claim 1; Fig 1A; 32pp; English.
XX
XX The present amino acid sequence is the mouse AF2 antibody, light chain
XX variable region (AF2-VL). It has IgG2b isotype and kappa light chain. It
XX is used for the construction of humanised version of mouse AF2 antibody
XX HuZAF, that comprises mouse antibody AF2 complementarity determining
XX regions (CDRs), functionally joined to the human acceptor antibody EU
XX framework region (FR). HuZAF antibody specifically binds to and
XX neutralises gamma-interferon (IFN). They can also block the binding of
XX mouse AF2 immunoglobulin to gamma-IFN. HuZAF does not contain sequences
XX that are immunogenically active in humans and remains unaffected by
XX immune responses, that may reduce its activity or circulating half-life.
XX HuZAF may be administered to treat autoimmune diseases such as graft
XX versus host disease following organ transplant, Type I diabetes, multiple
XX sclerosis, rheumatoid arthritis, psoriasis, systemic lupus erythematosus
XX (SLE), Hashimoto's thyroiditis, primary biliary cirrhosis and
XX inflammatory bowel disease like, Crohn's disease
XX
XX Sequence 127 AA;
XX
XX Query Match 92.7%; Score 521; DB 3; Length 127;
XX Best Local Similarity 91.6%; Pred. No. 1, 2e-35;
XX Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 NIVMTQSPKMSMSVGERVTLTKASENVTVVSWYQKPSQPKLLIYGASNRYTGVPD 60
XX 21 NIVMTQSPKMSMSVGERVTLTKASENVTVVSWYQKPSQPKLLIYGASNRYTGVPD 80
XX
XX 61 RFTGSGSATDFTLTISVQAEADLYHCGQGYSPYPTFGGKLEIK 107
XX 81 RFTGSGSATDFTLTISVQAEADLYHCGQGYSPYPTFGGKLEIK 127
XX
XX Search completed: August 16, 2004, 11:12:18
XX Job time : 47.5426 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 16, 2004, 11:08:07 ; Search time 13.9148 Seconds
(without alignments)
396.986 Million cell updates/sec

Title: US-09-889-300A-2

Perfect score: 562

Sequence: 1 NIVMTQSPKSNMSVGERVT.....CGQGYSPVTFGGTKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	100.0	107	3	US-08-838-682-16
2	562	100.0	107	3	US-08-838-682-16
3	562	100.0	107	3	US-08-838-682-16
4	562	100.0	107	4	US-08-838-682-16
5	562	100.0	109	5	US-08-838-682-16
6	562	100.0	121	3	US-08-838-682-16
7	562	100.0	121	3	US-08-838-682-16
8	562	100.0	121	3	US-08-838-682-16
9	562	100.0	121	4	US-08-838-682-16
10	521	92.7	127	4	US-08-838-682-16
11	521	92.7	136	1	US-08-838-682-16
12	521	92.7	136	1	US-08-838-682-16
13	521	92.7	136	1	US-08-838-682-16
14	521	92.7	136	1	US-08-838-682-16
15	521	92.7	136	3	US-08-838-682-16
16	454	80.8	107	3	US-08-838-682-16
17	454	80.8	107	4	US-08-838-682-16
18	454	80.8	107	4	US-08-838-682-16
19	449	79.9	107	3	US-08-838-682-16
20	449	79.9	107	4	US-08-838-682-16
21	449	79.9	107	4	US-08-838-682-16
22	447	79.5	107	3	US-08-838-682-16
23	447	79.5	107	4	US-08-838-682-16
24	447	79.5	107	4	US-08-838-682-16
25	444	79.0	107	3	US-08-838-682-16
26	444	79.0	107	4	US-08-838-682-16
27	444	79.0	107	4	US-08-838-682-16

28 441 78.5 107 1 US-07-634-278-103 Sequence 103, App
29 441 78.5 107 1 US-08-477-728-103 Sequence 103, App
30 441 78.5 107 1 US-08-474-040-103 Sequence 103, App
31 441 78.5 107 1 US-08-487-200-103 Sequence 103, App
32 441 78.5 107 3 US-08-484-537-103 Sequence 103, App
33 441 78.5 128 4 US-09-450-520A-6 Sequence 6, Appl
34 426 75.8 108 3 US-09-157-370-4 Sequence 4, Appl
35 424.5 75.5 108 2 US-08-557-012-25 Sequence 25, Appl
36 424.5 75.5 108 3 US-09-013-872-25 Sequence 25, Appl
37 424.5 75.5 108 4 US-09-184-198-25 Sequence 25, Appl
38 424.5 75.5 108 4 US-09-633-653-25 Sequence 25, Appl
39 424 75.4 249 2 US-08-797-689-18 Sequence 18, Appl
40 424 75.4 249 4 US-09-984-186-18 Sequence 18, Appl
41 423 75.3 108 3 US-08-752-693A-1 Sequence 1, Appl
42 423 75.3 132 1 US-08-253-877C-55 Sequence 55, Appl
43 423 75.3 132 2 US-08-452-164A-55 Sequence 36, Appl
44 423 75.3 132 4 US-08-976-183A-36 Sequence 37, Appl
45 423 75.3 132 4 US-08-976-183A-36 Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-08-838-682-16
; Sequence 16, Application US/08838682
; Patent No. 6107090
; GENERAL INFORMATION:
; APPLICANT: Bander M.D., Neill H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,682
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-682-16

Query Match 100.0%; Score 562; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.4e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMMSVGERVTITCKASENVVTWVSWYQKQKPEQSPKLLIYGASNRYTGVDP 60

Db 1 NIVMTQSPKSMMSVGERVTITCKASENVVTWVSWYQKQKPEQSPKLLIYGASNRYTGVDP 60

Qy 61 RFTGSGSATDFTLTIISSVQAEADLYHCQGQGSYPYTFGGGTKEIK 107
|||
Db 61 RFTGSGSATDFTLTIISSVQAEADLYHCQGQGSYPYTFGGGTKEIK 107

RESULT 2
US-08-895-914-16
; Sequence 16, Application US/08895914
; Patent No. 6136311
; GENERAL INFORMATION:
; APPLICANT: Bangder, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square P.O. Box 1051

Query Match	100.0%;	Score 562;	DB 3;	Length 107;
Best Local Similarity	100.0%;	Pred. No. 3.4e-50;		
Matches 107:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 NIVMTOSP KSM SMSGVGRVTITCKAENNVTVSWYQOKPQSPKLLIYGASNRVTGVPD 60

Qy 61 RFTGGSATDFTLTIISSVQAEADLYHCGQGSYPYTFGGGTKLEIK 107
| | | | |
Db 61 RFTGGSATDFTLTIISSVQAEADLYHCGQGSYPYTFGGGTKLEIK 107
| | | | |

RESULT 3

US-09-357-710A-16
; Sequence 16, Application US/09357710A
; Patent No. 6390956
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.

```
Query Match      100.0%; Score 562; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.4e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 NIVMTQSPKMSMSVGERVLTICKASENVVTYVSWYQQPEQSPKLLIYGASNRVTGVPD 60
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Db 1 NIVMTQSPKMSMSVGERVLTICKASENVVTYVSWYQQPEQSPKLLIYGASNRVTGVPD 60

Qy

61 RFTGSGSATDFTLTIISSVQAEDLADYHCGQGYSYPYTFGGGTKEIK 107
| | | | |
| | | | |

Dp

61 RFTGSGSATDFTLTIISSVQAEDLADYHCGQGYSYPYTFGGGTKEIK 107
| | | | |
| | | | |

RESULT 4
US-09-357-707-16
; Sequence 16, Application US/09357707
; Patent No. 6649163
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/078
; CURRENT APPLICATION NUMBER: US/09/357.707

Query Match	100.0%;	Score 562;	DB 4;	Length 107;
Best Local Similarity	100.0%;	Pred. No. 3.4e-50;		
Matches	107.	Conservative	0.	Mismatches 0.
				Indels

Qy 1 NIWVTQSPKSMGVGERVLTCKASENVTVTSWYQQPEQSPKLLIYGASNRVTGVDP 60

QY 61 RFTGSGSATFTLTISSVQAEADLYHCGQGYSPYTFGGGTXLEIK 107

RESULT 5

PCT-US92-02044-2
 ; Sequence 2, Application PC/TUS9202044
 ; GENERAL INFORMATION:
 ; APPLICANT: BIOGEN, INC.
 ; APPLICANT: SATO, Vicki L.
 ; APPLICANT: CHISHOLM, Patricia L.
 ; APPLICANT: WALGNER, Barbara P.
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES RECOGNIZING
 ; TITLE OF INVENTION: LYMPHOCYTE FUNCTION ASSOCIATED ANTIGEN-3
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: C/O FISH & NEAVE
 ; STREET: 875 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10022

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/02044
 FILING DATE: 19920312

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/667,975
 FILING DATE: 12-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: HALEY Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: B150CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 715-0600
 TELEFAX: (212) 715-0673

TELEX: 14-8367
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 109 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US92-02044-2

Query Match 100.0%; Score 562; DB 5; Length 109;
 Best Local Similarity 100.0%; Pred.No.3.5e-50;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMMSVGERVLTCKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
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 Db 1 NIVMTQSPKSMMSVGERVLTCKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
 |||||
 QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
 |||||
 Db 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
 |||||

RESULT 6

US-08-838-682-11
 ; Sequence 11, Application US/08838682
 ; Patent No. 6107090
 ; GENERAL INFORMATION:
 ; APPLICANT: Bander M.D., Neil H.
 ; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
 ; TITLE OF INVENTION: CANCER
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 ; STREET: Clinton Square, P.O. Box 1051

CITY: Rochester
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 14603-1051
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,682
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/016,976
 FILING DATE: 06-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/022,125
 FILING DATE: 18-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldman, Michael L.
 REGISTRATION NUMBER: 30,727
 REFERENCE/DOCKET NUMBER: 19603/1172
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (716) 263-1304
 TELEFAX: (716) 263-1600
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 121 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-682-11

Query Match 100.0%; Score 562; DB 3; Length 121;
 Best Local Similarity 100.0%; Pred.No.3.9e-50;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMMSVGERVLTCKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
 |||||
 Db 7 NIVMTQSPKSMMSVGERVLTCKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 66
 |||||
 QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
 |||||
 Db 67 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 113
 |||||

RESULT 7

US-08-895-914-11
 ; Sequence 11, Application US/08895914
 ; Patent No. 6136311
 ; GENERAL INFORMATION:
 ; APPLICANT: Bander, Neil H.
 ; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 ; STREET: Clinton Square, P.O. Box 1051
 ; CITY: Rochester
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 14603-1051
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/895,914
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/016,976
FILING DATE: 06-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-JUL-1996
PRIOR APPLICATION DATA: US 08/838,682
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1173
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-895-914-11

Query Match 100.0%; Score 562; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.9e-50; Mismatches 0; Indels 0; Gaps 0;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIWMTQSPKSMVSGERVTLTCKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 7 NIWMTQSPKSMVSGERVTLTCKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 66
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTTKLEIK 107
Db 67 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTTKLEIK 113

RESULT 8

US-09-357-710A-11
Sequence 11, Application US/09357710A
Patent No. 6290956
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: Lois M. Kwasigroch: BZL 242/025
CURRENT APPLICATION NUMBER: US/09/357,710A
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 08/838,682
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR FILING DATE: 1996-05-06
PRIOR APPLICATION NUMBER: US 60/022,125
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 121
TYPE: PRT
ORGANISM: Mus sp.
US-09-357-710A-11

Query Match 100.0%; Score 562; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.9e-50; Mismatches 0; Indels 0; Gaps 0;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIWMTQSPKSMVSGERVTLTCKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 7 NIWMTQSPKSMVSGERVTLTCKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 66
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTTKLEIK 107
Db 67 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTTKLEIK 113

RESULT 9

US-09-357-707-11
Sequence 11, Application US/09357707
Patent No. 6649163
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
FILE REFERENCE: Lois M. Kwasigroch: BZL 242/078
CURRENT APPLICATION NUMBER: US/09/357,707
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 08/895,914
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: US 08/838,682
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR FILING DATE: 1996-05-06
PRIOR APPLICATION NUMBER: US 60/022,125
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 121
TYPE: PRT
ORGANISM: Mus sp.
US-09-357-707-11

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Best Local Similarity 100.0%; Pred. No. 3.9e-50; Mismatches 0; Indels 0; Gaps 0;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 7 NIWMTQSPKSMVSGERVTLTCKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 66
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTTKLEIK 107
Db 67 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTTKLEIK 113

RESULT 10

US-09-450-520A-2
Sequence 2, Application US/09450520A
Patent No. 6329511
GENERAL INFORMATION:
APPLICANT: Vasquez, Maximiliano
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Tsurushita, Naoya
APPLICANT: Queen, Cary L.
TITLE OF INVENTION: Protein Design Labs, Inc.
FILE REFERENCE: 011823-008110US
CURRENT APPLICATION NUMBER: US/09/450,520A
CURRENT FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 60/110,523
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 127
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: AP2 VL
US-09-450-520A-2

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Best Local Similarity 91.6%; Pred. No. 6.2e-46; Mismatches 4; Indels 0; Gaps 0;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
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Db 21 NIWMTQSPKSMVSGERVTLTCKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 80

QY 61 RFTGSSATDFTLTSSVQAEADLADYHCGQGSYPYTFGGTKLEIK 107
Db 81 RFTGSSATDFTLTSSVQAEADLADYHCGQGSYPYTFGGTKLEIK 127

RESULT 11
US-07-634-278-99
; Sequence 99, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COSLINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-634-278-99

Query Match 92.7%; Score 521; DB 1; Length 136;
Best Local Similarity 91.6%; Pred. No. 6.8e-46;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 NIWMTQSPKSMMSVGERVTITCKASENVTVYSWYQQKPEQSPKLLIYGASNRYTGVPD 60
Db 30 NIWMTQSPKSMYSIGERVTLTSCASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89
QY 61 RFTGSSATDFTLTSSVQAEADLADYHCGQGSYPYTFGGTKLEIK 107
Db 90 RFTGSSATDFTLTSSVQAEADLADYHCGQGSYPYTFGGTKLEIK 136

RESULT 12

US-08-477-728-99
; Sequence 99, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-728-99

Query Match 92.7%; Score 521; DB 1; Length 136;
Best Local Similarity 91.6%; Pred. No. 6.8e-46;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 NIWMTQSPKSMMSVGERVTITCKASENVTVYSWYQQKPEQSPKLLIYGASNRYTGVPD 60
Db 30 NIWMTQSPKSMYSIGERVTLTSCASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89
QY 61 RFTGSSATDFTLTSSVQAEADLADYHCGQGSYPYTFGGTKLEIK 107
Db 90 RFTGSSATDFTLTSSVQAEADLADYHCGQGSYPYTFGGTKLEIK 136

RESULT 13
US-08-474-040-99
; Sequence 99, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600

TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-040-99

Query Match 92.7%; Score 521; DB 1; Length 136;
Best Local Similarity 91.6%; Pred. No. 6.8e-46;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSGERVTLTKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
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QY 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
Db 90 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGKLEIK 136

RESULT 14
US-08-487-200-99
Sequence 99, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610

TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-200-99

Query Match 92.7%; Score 521; DB 1; Length 136;
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Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Db 90 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGKLEIK 136

RESULT 15
US-08-484-537-99
Sequence 99, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto

STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US/07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-537-99

Query Match 92.7%; Score 521; DB 3; Length 136;
Best Local Similarity 91.6%; Pred. No. 6.8e-46;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
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Search completed: August 16, 2004, 11:12:58
Job time : 14.9148 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 16, 2004, 11:10:36 ; Search time 38.8655 Seconds
(without alignments)
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Title: US-09-889-300A-2

Perfect score: 562

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Searched: 1292805 seqs, 313927144 residues 1292805

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	562	100.0	121	10	US-09-929-665-11
4	562	100.0	121	10	US-09-929-546-11
5	562	100.0	128	14	US-10-010-729-70
6	562	100.0	132	13	US-10-006-773-19
7	562	100.0	135	12	US-10-372-481-31
8	562	100.0	135	15	US-10-371-797-31
9	554	98.6	128	8	US-08-779-784-34
10	534	95.0	107	14	US-10-010-729-21
11	521	92.7	127	9	US-09-992-524-2
12	512	91.1	136	12	US-10-389-417-84
13	512	91.1	136	12	US-10-452-357-99
14	512	91.1	136	15	US-10-389-155-84
15	503	89.5	107	14	US-10-160-506-48

16	503	89.5	107	16	US-10-449-379-48	Sequence 48, Appl
17	503	89.5	107	16	US-10-688-015-48	Sequence 48, Appl
18	490	87.2	107	14	US-10-160-506-64	Sequence 64, Appl
19	490	87.2	107	14	US-10-160-506-65	Sequence 65, Appl
20	490	87.2	107	16	US-10-449-379-64	Sequence 64, Appl
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22	490	87.2	107	16	US-10-688-015-64	Sequence 64, Appl
23	490	87.2	107	16	US-10-688-015-65	Sequence 65, Appl
24	487	86.7	107	14	US-10-160-506-66	Sequence 66, Appl
25	487	86.7	107	14	US-10-449-379-66	Sequence 66, Appl
26	487	86.7	107	16	US-10-688-015-66	Sequence 66, Appl
27	485	86.3	107	14	US-10-160-506-63	Sequence 63, Appl
28	485	86.3	107	16	US-10-449-379-63	Sequence 63, Appl
29	485	86.3	107	16	US-10-688-015-63	Sequence 63, Appl
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31	484	86.1	107	14	US-10-160-506-67	Sequence 67, Appl
32	484	86.1	107	14	US-10-160-506-68	Sequence 68, Appl
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36	484	86.1	107	16	US-10-688-015-50	Sequence 50, Appl
37	484	86.1	107	16	US-10-688-015-67	Sequence 67, Appl
38	484	86.1	107	16	US-10-688-015-68	Sequence 68, Appl
39	478	85.1	107	14	US-10-160-506-62	Sequence 62, Appl
40	478	85.1	107	16	US-10-449-379-62	Sequence 62, Appl
41	478	85.1	107	16	US-10-688-015-62	Sequence 62, Appl
42	472	84.0	124	14	US-10-160-506-57	Sequence 57, Appl
43	472	84.0	124	16	US-10-449-379-57	Sequence 57, Appl
44	472	84.0	124	16	US-10-688-015-57	Sequence 57, Appl
45	454	80.8	107	10	US-09-874-141-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-929-665-16

; Sequence 16, Application US/09929665

; Publication No. US20030003101A1

; GENERAL INFORMATION:

; APPLICANT: Bander, Neil H.

; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: Lois M. Kwasiroch; B2L 242/024

; CURRENT APPLICATION NUMBER: US/09/929,665

; CURRENT FILING DATE: 2001-08-13

; PRIOR APPLICATION NUMBER: 09/357,704

; PRIOR FILING DATE: 1999-07-20

; PRIOR APPLICATION NUMBER: US 08/838,682

; PRIOR FILING DATE: 1997-04-09

; PRIOR APPLICATION NUMBER: US 60/016,976

; PRIOR FILING DATE: 1996-05-06

; PRIOR APPLICATION NUMBER: US 60/022,125

; PRIOR FILING DATE: 1996-07-18

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 16

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Mus sp.

; US-09-929-665-16

Query Match 100.0%; Score 562; DB 10; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.6e-48;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 NIVMTQSPKSMVSGRVTLTCKASNNVTVYSWYQCKPEQSPKLLIYGASNNRYTGVDP 60

QY 61 RFTGSGSATDTFLTISSVQAEADLADYHCGQGYSPYTFGGTKLEIK 107

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US-09-929-546-16
; Sequence 16, Application US/09929546
; Publication No. US20030031673A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasiroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/929,546
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,708
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
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; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-546-16

Query Match      100.0%; Score 562; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.6e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 NIVMTQSPKSMVSGERVTLTCKASENVVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60

QY 61 RFTGSGSATDFTLTISSVQAEADLADYHCGQGYSPYTFGGGTKEIK 107
DB 61 RFTGSGSATDFTLTISSVQAEADLADYHCGQGYSPYTFGGGTKEIK 107

RESULT 3
US-09-929-665-11
; Sequence 11, Application US/09929665
; Publication No. US2003003101A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasiroch: BZL 242/024
; CURRENT APPLICATION NUMBER: US/09/929,665
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,704
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-665-11

Query Match      100.0%; Score 562; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.9e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSGERVTLTCKASENVVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
DB 1 NIVMTQSPKSMVSGERVTLTCKASENVVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60

QY 61 RFTGSGSATDFTLTISSVQAEADLADYHCGQGYSPYTFGGGTKEIK 107
DB 61 RFTGSGSATDFTLTISSVQAEADLADYHCGQGYSPYTFGGGTKEIK 107

RESULT 5
US-10-010-729-70
; Sequence 70, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
US-10-010-729-70

Query Match      100.0%; Score 562; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.9e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSGERVTLTCKASENVVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
DB 7 NIVMTQSPKSMVSGERVTLTCKASENVVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 66

QY 61 RFTGSGSATDFTLTISSVQAEADLADYHCGQGYSPYTFGGGTKEIK 107
DB 67 RFTGSGSATDFTLTISSVQAEADLADYHCGQGYSPYTFGGGTKEIK 113
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; SEQ ID NO 70
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-70

Query Match      100.0%; Score 562; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 2e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMMSVGERVTLTKASENNVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
DQ 21 NIVMTQSPKSMMSVGERVTLTKASENNVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 80
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 107
DQ 81 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 127

RESULT 6
US-10-006-773-19
; Sequence 19, Application US/10006773
; Publication NO. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-19

Query Match      100.0%; Score 562; DB 13; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMMSVGERVTLTKASENNVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
DQ 25 NIVMTQSPKSMMSVGERVTLTKASENNVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 84
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 107
DQ 85 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 131

RESULT 7
US-10-372-481-31
; Sequence 31, Application US/10372481
; Publication NO: US20030202975A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 5405.306
; CURRENT APPLICATION NUMBER: US/10/372,481
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05549
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-481-31

Query Match      100.0%; Score 562; DB 12; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMMSVGERVTLTKASENNVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
DQ 21 NIVMTQSPKSMMSVGERVTLTKASENNVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 80
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 107
DQ 81 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 127

RESULT 8
US-10-371-797-31
; Sequence 31, Application US/10371797
; Publication NO. US20040001828A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TUSCANO, Joseph
; APPLICANT: TEDDER, Thomas
; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 39754-0951
; CURRENT APPLICATION NUMBER: US/10/371,797
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 135
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-371-797-31

Query Match      100.0%; Score 562; DB 15; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMMSVGERVTLTKASENNVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
DQ 21 NIVMTQSPKSMMSVGERVTLTKASENNVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 80
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 107
DQ 81 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 127

RESULT 9
US-08-779-784-34
; Sequence 34, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; ORGANISM: Homo sapiens
US-08-779-784-34

Query Match      100.0%; Score 562; DB 15; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMMSVGERVTLTKASENNVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
DQ 21 NIVMTQSPKSMMSVGERVTLTKASENNVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 80
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 107
DQ 81 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 127
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; APPLICATION DATA: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-08-779-784-34

Query Match          98.6%; Score 554; DB 8; Length 128;
Best Local Similarity 99.1%; Pred. No. 1.3e-47;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIWMTQSPKSMVSIGERVTLTKASENVVTVSVWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 21 NIWMTQSPKSMVSIGERVTLTKASENVVTVSVWYQKPEQSPKLLIYGASNRYTGVPD 80

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGTKLEIK 107
Db 81 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGTKLEIK 127

RESULT 10
US-10-010-729-21
; Sequence 21, Application US/10010729
; Publication NO. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520

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; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-010-729-21

Query Match          95.0%; Score 534; DB 14; Length 101;
Best Local Similarity 100.0%; Pred. No. 9.6e-46;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIWMTQSPKSMVSIGERVTLTKASENVVTVSVWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 1 NIWMTQSPKSMVSIGERVTLTKASENVVTVSVWYQKPEQSPKLLIYGASNRYTGVPD 60

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGG 101
Db 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGG 101

RESULT 11
US-09-992-524-2
; Sequence 2, Application US/09992524
; Patent No. US20020091240A1
; GENERAL INFORMATION:
; APPLICANT: Vasquez, Maximiliano
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Queen, Cary L.
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
; FILE REFERENCE: 011823-008110US
; CURRENT APPLICATION NUMBER: US/09/992,524
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/450,520
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: AF2 VL
; US-09-992-524-2

Query Match          92.7%; Score 521; DB 9; Length 127;
Best Local Similarity 91.6%; Pred. No. 2.5e-44;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIWMTQSPKSMVSIGERVTLTKASENVVTVSVWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 21 NIWMTQSPKSMVSIGERVTLTKASENVVTVSVWYQKPEQSPKLLIYGASNRYTGVPD 80

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGTKLEIK 107
Db 81 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGTKLEIK 127

RESULT 12
US-10-389-417-84
; Sequence 84, Application US/10389417
; Publication NO. US20040049014A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William P.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Coeligh, Kathleen L.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins

```

NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,417
FILING DATE: 13-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US/07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US/07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US/07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US/08/484,537
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-389-417-84
Query Match 91.1%; Score 512; DB 12; Length 136;
Best Local Similarity 90.7%; Pred. No. 2.1e-43;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 NIVMTQSPKMSMSVGERVTLTKASENVTVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
DB 30 NIVMTQSPKMSVIGERVTLTKASENVTVTVSWYQKPEQSPKLLIYGASNRYTGVD 89
QY 61 RFTGSGSATDFTLTSSVQAEADLADYHCGGYSYPYTFGGTKLEIK 107
DB 90 RFTGSGSATDFTLTSSVQAEADLADYHCGGYSYNYPTFGSGTKLEIK 136
RESULT 13
US-10-452-357-99
Sequence 99, Application US/10452357
Publication No. US20040058414A1
GENERAL INFORMATION:
APPLICANT: Queen, Cary
APPLICANT: Co, Man Sung
APPLICANT: Schneider, William
APPLICANT: Landolfi, Nicholas
APPLICANT: Coelingh, Kathleen
APPLICANT: Selick, Harold
TITLE OF INVENTION: Improved Humanized Immunoglobulins
FILE REFERENCE: 05882.0078.CNUS01
CURRENT APPLICATION NUMBER: US/10/452,357

CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: 09/718,993
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 09/487,200
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/634,278
PRIOR FILING DATE: 1990-12-13
PRIOR APPLICATION NUMBER: 07/590,275
PRIOR FILING DATE: 1990-09-28
PRIOR APPLICATION NUMBER: 07/310,252
PRIOR FILING DATE: 1989-02-13
PRIOR APPLICATION NUMBER: 07/290,975
PRIOR FILING DATE: 1988-12-28
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn version 3.2
SEQ ID NO 99
LENGTH: 136
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: AF2 light chain antibody
US-10-452-357-99
Query Match 91.1%; Score 512; DB 12; Length 136;
Best Local Similarity 90.7%; Pred. No. 2.1e-43;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 NIVMTQSPKMSMSVGERVTLTKASENVTVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
DB 30 NIVMTQSPKMSVIGERVTLTKASENVTVTVSWYQKPEQSPKLLIYGASNRYTGVD 89
QY 61 RFTGSGSATDFTLTSSVQAEADLADYHCGGYSYPYTFGGTKLEIK 107
DB 90 RFTGSGSATDFTLTSSVQAEADLADYHCGGYSYNYPTFGSGTKLEIK 136
RESULT 14
US-10-389-155-84
Sequence 84, Application US/10389155
Publication No. US20030229208A1
GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
Co, Man Sung
Schneider, William P.
Landolfi, Nicholas F.
Coelingh, Kathleen L.
Selick, Harold E.
TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,155
FILING DATE: 13-Mar-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US/07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US/07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US/07/590,274
FILING DATE: 28-SEP-1990

APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-00265005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-389-155-84

Query Match 91.1%; Score 512; DB 15; Length 136;
Best Local Similarity 90.7%; Pred. No. 2.1e-43;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Qy 1 NIVMTQSPKSMMSGVGVTLTKCKASENVTVVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
Db 30 NIVMTQSPKSMYSIGERVTLCKASENVTVVSWYQQKPEQSPKLLIYGASNRYTGVD 89
Qy 61 RFTGSGSATDFTLTSSVQAEDLADYHCGQGSYPYTFGGGKLEIK 107
Db 90 RFTGSGSATDFTLTSSVQAEDLADYHCGQGSYPYTFGGGKLEIK 136

RESULT 15

US-10-160-506-48
Sequence 48, Application US/10160506
Publication No. US20030161832A1
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
FILE REFERENCE: 10448-162001
CURRENT APPLICATION NUMBER: US/10/160,506
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/324,100
PRIOR FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 60/362,612
PRIOR FILING DATE: 2002-03-08
NUMBER OF SEQ ID NOS: 128
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 48
LENGTH: 107
TYPE: PRT
ORGANISM: Mus musculus
US-10-160-506-48

Query Match 89.5%; Score 503; DB 14; Length 107;
Best Local Similarity 87.9%; Pred. No. 1.3e-42;
Matches 94; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Qy 1 NIVMTQSPKSMMSGVGVTLTKCKASENVTVVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
Db 1 NIVMTQSPKSMMSGVGVTLTKCKASENVTVVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
Qy 61 RFTGSGSATDFTLTSSVQAEDLADYHCGQGSYPYTFGGGKLEIK 107
Db 61 RFTGSGSATDFTLTSSVQAEDLADYHCGQGSYPYTFGGGKLEIK 107

Search completed: August 16, 2004, 11:21:20
Job time : 39.8655 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 16, 2004, 11:08:06 ; Search time 11.5157 Seconds
(without alignments)
893.780 Million cell updates/sec

Title: US-09-889-300A-2
Perfect score: 562
Sequence: 1 NIVMTQPKSMNSVGERVT.....CGQGYSPYTFGGGTKLEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	100.0	136	1 KWS21	Ig kappa chain pre
2	551	98.0	111	2 D37266	Ig kappa chain v r
3	515	91.6	107	2 S31132	Ig kappa chain v r
4	498	88.6	118	2 I33932	Ig kappa chain pre
5	494	87.9	107	2 S38713	Ig kappa chain v r
6	459	81.7	107	2 P10268	Ig kappa chain v r
7	454	80.8	96	2 P1070	Ig light chain v r
8	446.5	79.4	91	2 P1071	Ig light chain v r
9	440	78.3	108	2 P10204	anti-DNA autoantib
10	432	76.9	107	2 S32192	Ig kappa chain v r
11	429	76.3	117	2 S42466	Ig kappa chain v r
12	427	76.0	107	2 S32191	Ig kappa chain v r
13	422	75.1	149	1 KWS11	Ig kappa chain pre
14	419	74.6	127	2 S04577	Ig kappa chain pre
15	416	74.0	119	2 P00265	Ig kappa chain v r
16	410	73.0	107	2 A28195	Ig kappa chain v r
17	410	73.0	107	2 S68212	Ig kappa chain (Ma
18	409	72.8	152	2 S30751	Ig kappa chain pre
19	407	72.4	113	2 H30534	Ig kappa chain v r
20	407	72.4	131	2 P10207	anti-idiotypic ant
21	404	71.9	113	2 F30534	Ig kappa chain v r
22	403	71.7	114	1 KWS7A	Ig kappa chain v r
23	403	71.7	135	2 S38807	Ig light chain v-J
24	401	71.4	113	2 P10264	Ig kappa chain v r
25	398.5	70.9	225	2 S37484	Ig kappa chain - m
26	396	70.5	128	2 A47159	Ig lambda chain v
27	395	70.3	107	2 D53285	Ig kappa chain v a
28	395	70.3	112	2 E30538	Ig kappa chain v r
29	395	70.3	112	2 F30538	Ig kappa chain v r

RESULT 1
KWS21
Ig kappa chain precursor V region (MOPC 21) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence revision 02-Apr-1982 #text_change 22-Jun-1999
C:Accession: A93736; A90262; B49982; A01917
R:Hamlyn, P.H.; Gait, M.J.; Milstein, C.
Nucleic Acids Res. 9, 4485-4494, 1981
A:Title: Complete sequence of an immunoglobulin mRNA using specific priming and the did
A:Reference number: A93736; MUID:82059477; PMID:6170937
A:Accession: A93736
A:Molecule type: mRNA
A:Residues: 1-136 <HAM>
R:Swasti, J.; Milstein, C.
Biochem. J. 128, 427-444, 1972
A:Title: The complete amino acid sequence of a mouse kappa light chain.
A:Reference number: A90262; MUID:73053310; PMID:4638343
A:Contents: myeloma protein MOPC 21
A:Accession: A90262
A:Molecule type: protein
A:Residues: 30-136 <SVA>
R:Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.F.
J. Biol. Chem. 269, 2805-2813, 1994
A:Title: Topology of an amiloride-binding protein.
A:Reference number: A49982; MUID:94132051; PMID:8300613
A:Accession: B49982
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 30-136 <LIN>
A:Cross-references: GB:I24803; NID:G452098; PIDN:AAC37684.1; PID:G452099
A:Experimental source: clone BA7.1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka)
chain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into l
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-136/Product: Ig kappa chain V region (MOPC 21) #status experimental <MAT>
F:45-119/Domain: immunoglobulin homology <IMW>
F:125-136/Region: J segment (JK2)
F:152-117/Disulfide bonds: #status predicted

Query Match 100.0%; Score 562; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQPKSMNSVGERVTITCKASENVVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 30 NIVMTQPKSMNSVGERVTITCKASENVVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 89
QY 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIK 107
Db 90 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIK 136

RESULT 2

D37266
Ig kappa chain V region (129) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C/Accession: D37266
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A/Title: Heavy and light chain variable region sequences and antibody properties of anti
A/Reference number: A38740; MUID:91177923; PMID:1706720
A/Accession: D37266
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-111 <RUF>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 98.0%; Score 551; DB 2; Length 111;
Best Local Similarity 98.1%; Pred. No. 9.9e-42;
Matches 105; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIWMTQSPKSMVSGERVTLTCKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
:|||||
DB 4 DIWMTQIPKSMVSGERVTLTCKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 63
:|||||

QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
:|||||
DB 64 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 110
:|||||

RESULT 3

S33132
Ig kappa chain V region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C/Accession: S33132
R;Tempest, P.R.; Barbanti, E.; Bremner, P.; Carr, F.J.; Ghislieri, M.; Rifaldi, B.; Mar
submitted to the EMBL Data Library, May 1993
A/Description: A humanized anti-tumor necrosis factor alpha monoclonal antibody that act
A/Reference number: S33131
A/Accession: S33132
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-107 <TEM>
A/Cross-references: EMBL:222670; NID:g297473; PIDN:CAA80379.1; PID:g297474
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 91.6%; Score 515; DB 2; Length 107;
Best Local Similarity 92.5%; Pred. No. 1.4e-38;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 NIWMTQSPKSMVSGERVTLTCKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
:|||||
DB 1 NIWMTQSPKSMVSGERVTLTCKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
:|||||

QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
:|||||
DB 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
:|||||

RESULT 4

I33932
Ig kappa chain precursor V region (E7) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C/Accession: I33932
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989

A/Title: Two murine natural polyreactive autoantibodies are encoded by normutated ger
A/Reference number: A33932; MUID:9282823; PMID:2499887
A/Accession: I33932
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-118 <BAC>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:39-113/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 498; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 4.8e-37;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIWMTQSPKSMVSGERVTLTCKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
:|||||
DB 24 NIWMTQSPKSMVSGERVTLTCKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 83
:|||||
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPY 95
:|||||
DB 84 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPY 118
:|||||

RESULT 5

S38713
Ig light chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C/Accession: S38713
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A/Reference number: S38713
A/Accession: S38713
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-107 <CIM>
A/Cross-references: EMBL:X76019; NID:g416090; PIDN:CAA53606.1; PID:g13333952
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.9%; Score 494; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 9.8e-37;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 NIWMTQSPKSMVSGERVTLTCKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
:|||||
DB 1 DIVITQSPKSMVSGERVTLTCKASENVTVVSWYQKPEQSPKLLIYGASNRYTGVPD 60
:|||||
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
:|||||
DB 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
:|||||

RESULT 6

PL0268
Ig kappa chain V region (anti-DNA, DP9VK and DP17VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C/Accession: PL0268
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A/Reference number: PL0231; MUID:9011618; PMID:2104919
A/Accession: PL0268
A/Molecule type: mRNA
A/Residues: 1-107 <SHL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-107/Region: framework 4

Query Match 81.7%; Score 459; DB 2; Length 107;
Best Local Similarity 82.2%; Pred. No. 1.2e-33;
Matches 88; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSGRVTLTCKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPD 60
DB 1 NIVMAWSPKSMVSGRVTLTCKASENVGTTVSWYQKPEQSPKLLIYRASDRYFGVPD 60

QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTTKLEIK 107
DB 61 RFAAGSGAADFSLTISSVQAEADLADYHCGQGYSPYTFGGGTTKLEIK 107

RESULT 7
PH1070
IG light chain V region (clone 17s.5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1070
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1070
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-96 <TIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 454; DB 2; Length 96;
Best Local Similarity 93.9%; Pred. No. 2.9e-33;
Matches 92; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 1 NIVMTQSPKSMVSGRVTLTCKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPD 60
DB 1 NIVMTQSPKSMVSGRVTLTCKASENVGTTVSWYQKPEQSPKLLIYGASNRVTGVPD 60

QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTF 98
DB 61 RFTGSGSATDFTLTISVQAEADLADYHCGQ-YS-PTTF 96

RESULT 8
PH1071
IG light chain V region (clone 165.3m) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1071
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1071
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-91 <TIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 446.5; DB 2; Length 91;
Best Local Similarity 93.5%; Pred. No. 1.3e-32;
Matches 86; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 7 SPKSMVSGRVTLTCKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPDRFTGSG 66
DB 1 SPKSMVSGRVTLTCKASENVGTTVSWYQKPEQSPKLLIYGASNRVTGVPDRFTGSG 59

QY 67 SATDFTLTISVQAEADLADYHCGQGYSPYTF 98
DB 60 SATDFTLTISVQAEADLADYHCGQGYSPYTF 91

RESULT 9
PL0204
anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: PL0204
R:Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from 1
A:Reference number: PL0198; MUID:90309768; PMID:2114528
A:Accession: PL0204
A:Molecule type: mRNA
A:Residues: 1-108 <SMI>
A:Cross-references: CB:X53644; NID:G50198; PIDN:CAA37695.1; PID:G930144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:50-56/Region: complementarity-determining 2
F:89-97/Region: complementarity-determining 3
F:96-108/Region: JH region

Query Match 78.3%; Score 440; DB 2; Length 108;
Best Local Similarity 79.4%; Pred. No. 5.5e-32;
Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSGRVTLTCKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPD 60
DB 1 DIVMTQSKFMSTSVGRVSVTCKASQNVNTYVAVTQKPGQSPKALIYSASRYTGVPD 60

QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTTKLEIK 107
DB 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTTKLEIK 107

RESULT 10
S32192
IG kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S32192
R:izui, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32195
A:Accession: S32192
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <IZU>
A:Cross-references: EMBL:X70097; NID:G288262; PIDN:CAA49701.1; PID:G288263
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 432; DB 2; Length 107;
Best Local Similarity 79.4%; Pred. No. 2.8e-31;
Matches 85; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSGRVTLTCKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPD 60
DB 1 DIVMTQSKFMSTSVGRVSVTCKASQDVSTAVAVTQKPGQSPKALIYSASRYTGVPD 60

QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTTKLEIK 107
DB 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTTKLEIK 107

RESULT 11

S42466
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42466
R;Shiyarov, P.A.; Bessalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42466
A:Accession: S42466
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X78108; NID:G460824; PIDN:CAA54998.1; PID:G460825
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 429; DB 2; Length 117;
Best Local Similarity 78.5%; Pred. No. 5.5e-31;
Matches 84; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMGSGERVTLTKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
DB 11 DIVMTQSHKFMSTVSGDRVSIITCKASQDVSTAVAWYQKPGQSPKLLIYWASTRHTGVPD 70
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGTTKLEIK 107
DB 71 RFTGSGSGTDFTLTISVQAEADLADYHCGQGYSPYPTFGGTTKLEIK 117

RESULT 12

S32191
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S32191
R;Izui, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32185
A:Accession: S32191
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <IZU>
A:Cross-references: EMBL:X70095; NID:G288260; PIDN:CAA49700.1; PID:G288261
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 427; DB 2; Length 107;
Best Local Similarity 78.5%; Pred. No. 7.6e-31;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMGSGERVTLTKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
DB 1 DIVMTQSHKFMSTVSGDRVSIITCKASQDVSTAVAWYQKPGQSPKLLIYSASRYTGVDP 60
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGTTKLEIK 107
DB 61 RFTGSGSGTDFTLTISVQAEADLADYHCGQGYSPYPTFGGTTKLEIK 107

RESULT 13

KWMS11
Ig kappa chain precursor V region (MPC11) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 21-Jan-2000
C:Accession: A90823; A90753; A90298; A01916
R;Kelley, D.E.; Coleclough, C.; Perry, R.P.
Cell 29, 681-689, 1982
A:Title: Functional significance and evolutionary development of the 5'-terminal regions
A:Reference number: A90823; MUID:83001944; PMID:6288267

A:Accession: A90823

A:Molecule type: DNA
A:Residues: 1-71 <KEL>
A>Note: the sequence was determined from the differentiated gene
R;Rabbits, T.H.; Hamlyn, P.H.; Matthysens, G.; Roe, B.A.
Can. J. Biochem. 58, 176-187, 1980
A:Title: The variability, arrangement, and rearrangement of immunoglobulin genes.
A:Reference number: A90753; MUID:80176554; PMID:6245773
A:Accession: A90753
A:Molecule type: mRNA
A:Residues: 41-149 <RAB>
R;Smith, G.P.
Biochem. J. 171, 337-347, 1978
A:Title: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma MPC
A:Reference number: A90298; MUID:78186617; PMID:418775
A:Contents: myeloma protein MPC11
A:Accession: A90298
A:Molecule type: protein
A:Residues: 30-149 <SMI>
A>Note: the amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were not
C:Comment: The mature chain has 12 additional residues at its amino end, due to a tan
42 corresponds to the amino-terminal residue of typical kappa chains.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: duplication; heterotetramer; immunoglobulin
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-149/Product: Ig kappa chain V region (MPC11) #status experimental <MAT>
F:57-131/Domain: immunoglobulin homology <IMM>
F:64-129/Disulfide bonds: #status predicted

Query Match 75.1%; Score 422; DB 1; Length 149;
Best Local Similarity 78.5%; Pred. No. 2.9e-30;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMGSGERVTLTKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
DB 42 DIVMTQSHKFMSTVSGDRVSIITCKASQDVSTAVAWYQKPGQSPKLLIYSASRYTGVDP 101

QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGTTKLEIK 107
DB 102 RFTGSGSGTDFTLTISVQAEADLADYHCGQGYSPYPTFGGTTKLEIK 148

RESULT 14

S04577
Ig kappa chain precursor V region (MRL-RF28L) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: S04577
R;Kofler, R.; Duchosal, M.A.; Dixon, F.J.
submitted to the EMBL Data Library, March 1989
A:Description: Complexity, polymorphism and connectivity of murine V(kappa) gene fami-
A:Reference number: S04577
A:Accession: S04577
A:Molecule type: mRNA
A:Residues: 1-127 <KOF>
A:Cross-references: EMBL:X14622; NID:G52400; PIDN:CAA32775.1; PID:G52401
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-127/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 419; DB 2; Length 127;
Best Local Similarity 75.7%; Pred. No. 4.5e-30;
Matches 81; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMGSGERVTLTKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
DB 21 DIVMTQTPKFLPSAGDRVMTCKASQSGVGNVAVWYQKPGQSPKLLIYASNRVTGVPD 80
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGTTKLEIK 107

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 16, 2004, 11:08:06 ; Search time 7.67713 Seconds
(without alignments)
725.728 Million cell updates/sec

Title: US-09-889-300A-2
Perfect score: 562
Sequence: 1 NIVMTQSPKSMYSVGERVT.....CGQGYSPYTRGGGKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	562	100.0	136	1	KV5B_MOUSE
2	422	75.1	149	1	KV5A_MOUSE
3	403	71.7	114	1	KV1A_MOUSE
4	383	68.1	114	1	KV4A_HUMAN
5	376	66.9	134	1	KV4C_HUMAN
6	375	66.7	108	1	KV1M_HUMAN
7	370	65.8	108	1	KV1V_HUMAN
8	365	64.9	108	1	KV1O_HUMAN
9	363	64.6	108	1	KV1V_HUMAN
10	362.5	64.5	133	1	KV4B_HUMAN
11	359	63.9	108	1	KV1H_HUMAN
12	359	63.9	111	1	KV3J_MOUSE
13	359	63.9	129	1	KV1X_HUMAN
14	358	63.7	108	1	KV1L_HUMAN
15	358	63.7	111	1	KV3H_MOUSE
16	358	63.7	129	1	KV1W_HUMAN
17	357	63.5	108	1	KV1N_HUMAN
18	356.5	63.4	129	1	KV3M_HUMAN
19	355.5	63.3	129	1	KV3L_HUMAN
20	354	63.0	131	1	KV3I_MOUSE
21	353	62.8	108	1	KV1E_HUMAN
22	353	62.8	111	1	KV3L_MOUSE
23	352.5	62.7	109	1	KV3B_HUMAN
24	352.5	62.7	109	1	KV3F_HUMAN
25	350	62.3	108	1	KV1A_HUMAN
26	349.5	62.2	109	1	KV3E_HUMAN
27	349	62.1	108	1	KV1K_HUMAN
28	349	62.1	108	1	KV1P_HUMAN
29	348	61.9	108	1	KV1B_HUMAN
30	348	61.9	108	1	KV1S_HUMAN
31	348	61.9	108	1	KV5M_HUMAN
32	347	61.7	108	1	KV1R_HUMAN
33	344.5	61.3	129	1	KV3H_HUMAN
					P01634 mus musculus
					P01633 mus musculus
					P01632 mus musculus
					P01625 homo sapien
					P06314 homo sapien
					P01605 homo sapien
					P03062 homo sapien
					P01607 homo sapien
					P04430 homo sapien
					P01600 homo sapien
					P01662 mus musculus
					P04432 homo sapien
					P01604 homo sapien
					P01660 mus musculus
					P04431 homo sapien
					P01606 homo sapien
					P18136 homo sapien
					P18135 homo sapien
					P01661 mus musculus
					P01597 homo sapien
					P01664 mus musculus
					P01620 homo sapien
					P01624 homo sapien
					P01593 homo sapien
					P01623 homo sapien
					P01603 homo sapien
					P01608 homo sapien
					P01594 homo sapien
					P01611 homo sapien
					P01646 mus musculus
					P01610 homo sapien
					P04207 homo sapien

Query Match

100.0%; Score 562; DB 1; Length 136;

34 343.5 61.1 109 1 KV3D_HUMAN P01622 homo sapien
35 343 61.0 111 1 KV3K_MOUSE P01663 mus musculus
36 342.5 60.9 113 1 KV2G_MOUSE P01631 mus musculus
37 342 60.9 108 1 KV1G_HUMAN P01599 homo sapien
38 342 60.9 108 1 KV1Q_HUMAN P01609 homo sapien
39 342 60.9 108 1 KV5J_MOUSE P04946 mus musculus
40 342 60.9 111 1 KV3M_MOUSE P01665 mus musculus
41 341 60.7 108 1 KV1C_HUMAN P01595 homo sapien
42 341 60.7 108 1 KV5K_MOUSE P01644 mus musculus
43 339.5 60.4 108 1 KV3A_HUMAN P01619 homo sapien
44 339 60.3 111 1 KV3D_MOUSE P03977 mus musculus
45 339 60.3 111 1 KV3O_MOUSE P01667 mus musculus

ALIGNMENTS

RESULT 1
KV5B_MOUSE
ID KV5B_MOUSE STANDARD; PRT; 136 AA.
AC P01634;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-V region MOPC 21 precursor.
OS mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Galt M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [2]
RP SEQUENCE OF 30-136.
RX MEDLINE=7305310; PubMed=4638343;
RA Svasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00810; CAA24192.1; ALT_TERM.
DR PIR; A93736; KWS21.
DR FDB; IIGC; 03-JUN-95.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin v region; Signal; 3D-structure.
FT SIGNAL 1
FT CHAIN 30 136
FT DOMAIN 30 52 IG KAPPA CHAIN V-V REGION MOPC 21.
FT FRAMEWORK-1
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 53 63
FT FRAMEWORK-2
FT DOMAIN 64 78
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 85
FT FRAMEWORK-3
FT DOMAIN 86 117
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 126
FT FRAMEWORK-4
FT DOMAIN 127 136
FT NON TER 136
SQ SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;

Best Local Similarity 100.0%; Pred. No. 7e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMSSVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60
DB 30 NIVMTQSPKSMSSVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 89
QY 61 RFTGSGSATDFTLTSSVQAEADLYHCGQGYSPYTFGGGKLEIK 107
DB 90 RFTGSGSATDFTLTSSVQAEADLYHCGQGYSPYTFGGGKLEIK 136

RESULT 2
KVSA_MOUSE
ID KVSA_MOUSE STANDARD; PRT; 149 AA.
AC P01633;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MPC11 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE OF 1-71 FROM N.A.
RP MEDLINE=83001944; PubMed=6288267;
RA Kelley D.E., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the
RT 5'-terminal regions of immunoglobulin variable-region genes.";
RL Cell 29:681-689(1982).
[2]
RN SEQUENCE OF 41-149 FROM N.A.
RP MEDLINE=80176554; PubMed=6245773;
RA Rabbitts T.H., Hamlyn P.H., Matthysens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RT genes.";
RL Can. J. Biochem. 58:176-187(1980).
[3]
RN SEQUENCE OF 30-149.
RP MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT myeloma MPC 11.";
RL Biochem. J. 171:337-347(1978).
CC -!- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.

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EMBL; J00561; AAA38776.1; -
PIR; A90823; KMS11.
HSSP; P80362; 1WT1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; Igv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; Repeat.
SIGNAL 1 29
CHAIN 30 149 IG KAPPA CHAIN V-V REGION MPC11.
FT DOMAIN 42 64 FRAMEWORK-1.
FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 76 90 FRAMEWORK-2.
FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 98 129 FRAMEWORK-3.
FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 139 148 FRAMEWORK-4.
FT REPEAT 26 35
FT REPEAT 38 47
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match 75.1%; Score 422; DB 1; Length 149;
Best Local Similarity 78.5%; Pred. No. 6.2e-38;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMSSVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60
DB 42 DIVMTQSHKFMSTSVGDRVSIITCKASQDVSTTVAVYQKPKQSPKLLIYGASRYTGVPD 101
QY 61 RFTGSGSATDFTLTSSVQAEADLYHCGQGYSPYTFGGGKLEIK 107
DB 102 RFTGSGSGTDFTTTSSVQAEADLYHCGQGYSPYTFGGGKLEIK 148

RESULT 3
KVIA_MOUSE
ID KVIA_MOUSE STANDARD; PRT; 114 AA.
AC P01632;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region SI07A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=81241357; PubMed=6788990;
RA Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
RT chains.";
RL J. Exp. Med. 153:1366-1370(1981).

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EMBL; U29423; AAC00033.1; -
PIR; A01915; KVM57A.
HSSP; P01607; 1REI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; Igv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
KVIA_MOUSE 1 23
FT DOMAIN 24 40
FT DOMAIN 41 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 62 FRAMEWORK-2.
FT DOMAIN 63 94 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 95 103 FRAMEWORK-3.
FT DOMAIN 104 113 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 94
FT NON_TER 114 114 BY SIMILARITY.
SQ SEQUENCE 114 AA; 12717 MW; 32008EC8E9DBE67B CRC64;

Query Match 71.7%; Score 403; DB 1; Length 114;
Best Local Similarity 67.3%; Pred. No. 4.8e-36;
Matches 76; Conservative 16; Mismatches 15; Indels 6; Gaps 1;

QY 1 NIWMTQSPKMSVSGRVTLTCKASENV-----VTYUSWYQKPEQSPKLLIYGASNR 54
 Db 1 DIVMTQSPFLAVTASKKVTISCTASELSYSSKHVYLAWYQKPEQSPKLLIYGASNR 60
 QY 55 YTGVPDRFTGSGSATDFTLTISVQAEDLADYHCGGYSYPTFGGKLEIK 107
 Db 61 YIGVDPDRFTGSGSGTDFTLTISVQVEDLTHYCAQFYSYPLTFGAGTKLEIK 113

RESULT 4
 KV4A_HUMAN
 ID KV4A_HUMAN STANDARD; PRT; 114 AA.
 AC P01625;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-IV region Len.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE

RP MEDLINE=76004342; PubMed=50995;
 RA Schneider M., Hilschmann N.;
 RT "The primary structure of a monoclonic immunoglobulin-L-chain of
 RT subgroup IV of the kappa type (Bence-Jones protein Len).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557 (1975).
 RN [2]
 RP REVISION TO 9.
 RA Salomon A.;
 RL Submitted (AUG-1996) to Swiss-Prot.
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: This is a Bence-Jones protein.

DR PDB; 1BEQ; 01-FEB-01.
 DR PDB; 1LEU; 03-FEB-01.
 DR PDB; 1EFQ; 09-FEB-01.
 DR PDB; 1EK3; 06-MAR-01.
 DR PDB; 1LVE; 21-JAN-98.
 DR PDB; 3LVE; 18-MAY-99.
 DR PDB; 3LVE; 28-MAR-01.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23
 FT DOMAIN 24 40
 FT DOMAIN 41 55
 FT DOMAIN 56 62
 FT DOMAIN 63 94
 FT DOMAIN 95 101
 FT DOMAIN 102 113
 FT DISULFID 23 94
 FT NON TER 114 114
 SQ SEQUENCE 114 AA; 12640 MW; 0647FD17F236485 CRC64;

Query Match 68.1%; Score 383; DB 1; Length 114;
 Best Local Similarity 65.5%; Pred. No. 6.4e-34;
 Matches 74; Conservative 18; Mismatches 15; Indels 6; Gaps 1;

QY 1 NIWMTQSPKMSVSGRVTLTCKASENV-----VTYUSWYQKPEQSPKLLIYGASNR 54
 Db 1 DIVMTQSPDLAVSLGERATINCKSSQSVLYSSKNYLAWYQKFGPPKLLIYWASTR 60
 QY 55 YTGVPDRFTGSGSATDFTLTISVQAEDLADYHCGGYSYPTFGGKLEIK 107
 Db 61 ESGVDPDRFSGSGSGTDFTLTISLQAEADVAVYCCQYVSTPYSGGKLEIK 113

RESULT 5
 KV4C_HUMAN
 ID KV4C_HUMAN STANDARD; PRT; 134 AA.
 AC P06314;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-IV region B17 precursor.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041854; PubMed=2997713;
 RA Marsh P., Mills F., Gould H.;
 RT "Detection of a unique human V kappa IV germline gene by a cloned
 RT cDNA probe.";
 RL Nucleic Acids Res. 13:6531-6544 (1985).
 RN [2]
 RP REVISION TO 76.
 RA Marsh P.;
 RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

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DR EMBL; X02990; CAA26733.1; -.
 DR HSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 61 75 FRAMEWORK-2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 83 114 FRAMEWORK-3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 122 133 FRAMEWORK-4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON TER 134 134
 SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 66.9%; Score 376; DB 1; Length 134;
 Best Local Similarity 62.8%; Pred. No. 4.3e-33;
 Matches 71; Conservative 21; Mismatches 15; Indels 6; Gaps 1;

QY 1 NIWMTQSPKMSVSGRVTLTCKASENV-----TVSWYQKPEQSPKLLIYGASNR 54
 Db 21 DIVMTQSPDLAVSLGERATINCKSSQSVLYSSKNYLAWYQKFGPPKLLIYWASTR 80
 QY 55 YTGVPDRFTGSGSATDFTLTISVQAEDLADYHCGGYSYPTFGGKLEIK 107
 Db 81 ESGVDPDRFSGSGSGTDFTLTISLQAEADVAVYCCQYVSTPYSGGKLEIK 133

RESULT 6
 KVIM_HUMAN
 ID KVIM_HUMAN STANDARD; PRT; 108 AA.

DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region Rei.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
and characterization of the tryptic peptides; the complete amino acid
sequence of the protein; a contribution to the elucidation of the
three-dimensional structure of antibodies, in particular their
combining site."; Physiol. Chem. 356:167-191(1975).
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
of the Bence-Jones protein Rei refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURE.
DR PDB; 1REI; 17-FEB-84.
DR PDB; 1AR2; 12-NOV-97.
DR PDB; 1BWW; 29-DEC-99.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23
FT STRAND 4 7
FT TURN 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT STRAND 108 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E9143E1188BCE2A CRC64;
Query Match 64.9%; Score 365; DB 1; Length 108;
Best Local Similarity 63.2%; Pred. No. 5e-32;

Matches 67; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
QY 1 NIVMTQSPKSMVSGRVTITCKASENVVTVYISWYQOKEQSPKLLIYGASNRYTGVPD 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 DIQMTQSPSSLSASVGRVITTCASQDIKILNWNYYQQTGFKAPKLLIYASNLQAGVPS 60
QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYPYTFGGGTGLEI 106
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 RFGSGSGTDTFTTISLQPEDIATYICQQYQSLPYTFGGGTGLQI 106
RESULT 9
KV4B HUMAN
ID KV4B HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHJEN.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23
FT STRAND 24 34
FT TURN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;
Query Match 64.6%; Score 363; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 8.1e-32;
Matches 68; Conservative 17; Mismatches 22; Indels 0; Gaps 0;
QY 1 NIVMTQSPKSMVSGRVTITCKASENVVTVYISWYQOKEQSPKLLIYGASNRYTGVPD 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 DIQMTQSPSSLSASVGRVITTCASQDIKILNWNYYQQTGFKAPKLLIYASNLQAGVPS 60
QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYPYTFGGGTGLEI 107
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 NFGTSGSGTDFLTITISLQPEDIATYICQQYQSLPYTFGGGTGLQI 107
RESULT 10
KV4B HUMAN
ID KV4B HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region JI precursor.
OS Homo sapiens (Human).
Query Match 64.9%; Score 365; DB 1; Length 108;
Best Local Similarity 63.2%; Pred. No. 5e-32;

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combrato G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
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CC -----
DR EMBL; Z00022; CAA77317.1; -.
DR PIR; A01904; K4HUJ1.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; Ig_v.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 20 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 133 FRAMEWORK-1.
FT DOMAIN 21 43 FRAMEWORK-2.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON TER 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 64.5%; Score 362.5; DB 1; Length 133;
Best Local Similarity 63.7%; Pred. No. 1.2e-31;
Matches 72; Conservative 19; Mismatches 15; Indels 7; Gaps 2;

QY 1 NIWVTSQPKSMSSVGERVLTCTKASENVV-----TVSVYQKPEQSPKLLIYGASNR 54
Db 21 DIWVTSQPDLSVLSGERATNCKSQSVLYSNKNVLAWYQKPGQPPKLLIYWASTR 80
QY 55 YTGVPDRFTGSGSATFTLTISVQAEADLYHCGQGYSPYTFGGGTKLEIK 107
Db 81 ESGVPRFSGSGSDTFTLTISLSQAEADVAVYCCQYDTP-TFGGKTKEIK 132

RESULT 11
KV1H HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;

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RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01868; K1HUHU.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; Ig_v.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 FRAMEWORK-2.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 63.9%; Score 359; DB 1; Length 108;
Best Local Similarity 61.7%; Pred. No. 2.2e-31;
Matches 66; Conservative 22; Mismatches 19; Indels 0; Gaps 0;

QY 1 NIWVTSQPKSMSSVGERVLTCTKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60
Db 1 DIWVTSQPDLSVLSGERATNCKSQSVLYSNKNVLAWYQKPGQPPKLLIYAASLPSGVPS 60
QY 61 RTGSGSATFTLTISVQAEADLYHCGQGYSPYTFGGGTKLEIK 107
Db 61 RFSGSGSDTFTLTISLSQAEADVAVYCCQYDTP-TFGGKTKEIK 107

RESULT 12
KV3J MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
CC -I- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
CC HSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; Ig_v.
DR PROSITE; PS00835; IG_LIKE; 1.

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DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 29 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match
Best Local Similarity 63.9%; Score 359; DB 1; Length 111;
Matches 70; Conservative 17; Mismatches 20; Indels 4; Gaps 1;

QY 1 NIVMTQSPKSMVSGRVTLTCKASENVVTVYVSWYQOQPEQSPKLLIYGASNRVT 56
DB 1 NIVLTQSPASVAVSLGORATISCRASEVDSYGNFMHWYQOQPEQSPKLLIYASNL 60
QY 57 GVPDRFTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107
DB 61 GVPARFSGSGRDTFTLTIDVFEADDAATYCCQNNEDPTTFGGGKLEIK 111

RESULT 13
KVIX HUMAN STANDARD; PRT; 129 AA.
AC P04432;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region Daudi precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G.; Combratio G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC -----
DR EMBL; X00966; CAA25478.1; ALT_TERM.
DR PIR; A01884; KIHU01.
DR HSP; P0362; LWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
COMPLEMENTARITY-DETERMINING-2.
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FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 110
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7B5574C8 CRC64;

Query Match
Best Local Similarity 59.8%; Score 359; DB 1; Length 129;
Matches 64; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSGRVTLTCKASENVVTVYVSWYQOQPEQSPKLLIYGASNRVTGVPD 60
DB 23 DIQMTQSPSLASVGRVTITCRAGHNITNLSVYQQRPGRAPILLIYAVSNLQGVPS 82
QY 61 RFTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107
DB 83 RFGSGSGAEFTLTISLQPEDFATYCCQNYNFSFTFGGKVDNK 129

RESULT 14
KVIL HUMAN STANDARD; PRT; 108 AA.
AC P01604;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region Kue.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79237924; PubMed=112021;
RA Eulitz M.; Kley H.-P.; Zeitler H.-J.;
RT "The primary structure of the Bence-Jones protein Kue. The amino acid
RT sequence of the variable part of a human L-chain of the kappa-type."
RL Hoppe-Seidler's Z. Physiol. Chem. 360:725-734(1979).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01870; KIHUKU.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;

Query Match
Best Local Similarity 63.7%; Score 358; DB 1; Length 108;
Matches 66; Conservative 20; Mismatches 21; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSGRVTLTCKASENVVTVYVSWYQOQPEQSPKLLIYGASNRVTGVPD 60
DB 1 DIQMTQSPSTQFASVGRVTITCRASQINIMLAWYQOQPEKAPKLLIYKASTLETGVP 60
QY 61 RFTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107
```


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OM protein - protein search, using sw model

Run on: August 16, 2004, 11:08:06 ; Search time 31.6682 Seconds

(without alignments)
1066.069 Million cell updates/sec

Title: US-09-889-300A-2

Perfect score: 562

Sequence: 1 NIVMTQSPKSMVSGRVT.....CGQGYSPYTFGGGPKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	406	72.2	108	11 Q8VIJ0	Q8VIJ0 mus musculus
2	378	67.3	99	11 Q9JL74	Q9JL74 mus musculus
3	370.5	65.9	107	4 Q968A9	Q968A9 homo sapien
4	369	65.7	108	4 Q9UL77	Q9UL77 homo sapien
5	366.5	65.2	109	4 Q9UL78	Q9UL78 homo sapien
6	366	65.1	107	11 Q9ER29	Q9ER29 mus musculus
7	363.5	64.7	109	4 Q9UL85	Q9UL85 homo sapien
8	363.5	64.7	238	11 Q99M37	Q99M37 mus musculus
9	358	63.7	234	4 Q7Z473	Q7Z473 homo sapien
10	357	63.5	108	4 Q9UL79	Q9UL79 homo sapien
11	357	63.5	236	4 Q7Z3Y4	Q7Z3Y4 homo sapien
12	354	63.0	108	4 Q9UL70	Q9UL70 homo sapien
13	351.5	62.5	107	4 Q9UL81	Q9UL81 homo sapien
14	350.5	62.4	238	11 Q8VC16	Q8VC16 mus musculus
15	347.5	61.8	239	11 Q8VC55	Q8VC55 mus musculus
16	347	61.7	108	4 Q9UL83	Q9UL83 homo sapien

17	347	61.7	236	11 Q7TMK3	Q7TMK3 mus musculus
18	346.5	61.7	112	11 Q8KIF3	Q8KIF3 mus musculus
19	345	61.4	111	11 Q920E9	Q920E9 mus musculus
20	342.5	60.9	114	11 Q8KIF1	Q8KIF1 mus musculus
21	342	60.9	236	11 Q7TS98	Q7TS98 mus musculus
22	339.5	60.4	109	4 Q9UL86	Q9UL86 homo sapien
23	338	60.1	214	11 Q9RIAS	Q9RIAS mus musculus
24	337	60.0	234	11 Q9LWF8	Q9LWF8 mus musculus
25	336.5	59.9	134	11 Q8VDD0	Q8VDD0 mus musculus
26	335	59.6	237	13 Q7S236	Q7S236 xenopus lae
27	333	59.3	111	11 Q8L1U6	Q8L1U6 mus musculus
28	332	59.1	109	11 Q920E6	Q920E6 mus musculus
29	331.5	59.0	112	11 Q8KIF2	Q8KIF2 mus musculus
30	331	58.9	298	11 Q9QV20	Q9QV20 mus musculus
31	330	58.7	116	4 Q96P56	Q96P56 homo sapien
32	329.5	58.6	104	11 Q9JL82	Q9JL82 mus musculus
33	329.5	58.6	243	11 Q7TOM2	Q7TOM2 mus musculus
34	329	58.5	233	11 Q9LWS9	Q9LWS9 mus musculus
35	328.5	58.5	106	5 Q9U410	Q9U410 schistosoma
36	326.5	58.1	239	4 Q8NEK0	Q8NEK0 homo sapien
37	325	57.8	234	11 Q8RO62	Q8RO62 mus musculus
38	324.5	57.7	239	4 Q8TCD0	Q8TCD0 homo sapien
39	323	57.5	234	11 Q8VCP0	Q8VCP0 mus musculus
40	321	57.1	131	11 Q8L1C3	Q8L1C3 mus musculus
41	316.5	56.3	235	11 Q7TMK0	Q7TMK0 mus musculus
42	313	55.7	109	6 Q9N0W5	Q9N0W5 oryctolagus
43	313	55.7	114	4 Q9UL80	Q9UL80 homo sapien
44	311.5	55.4	239	11 Q8KOF8	Q8KOF8 mus musculus
45	309	55.0	101	11 Q9JL78	Q9JL78 mus musculus

ALIGNMENTS

RESULT 1

Q8VIJ0 Q8VIJ0 PRELIMINARY; PRT; 108 AA.

ID Q8VIJ0; 01-VAR-2002 (TREMELrel. 20, Created)
DT 01-VAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Anti-DNA light chain (fragment).
GN VK19.

CS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C3H/HeJ-lpr/lpr;

RX MEDLINE=96409289; PubMed=8814271;

RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;

RT "Differences in V kappa gene utilization and VH CDR3 sequence among

anti-DNA from C3H-lpr mice and lupus mice with nephritis.";

RL Eur. J. Immunol. 26:2225-2233 (1996).

DR EMBL; U59155; AAB02917.1; -

DR PIR; A33933; A33933.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 108

SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 72.2%; Score 406; DB 11; Length 108;

Best Local Similarity 74.8%; Pred. No. 2.6e-36;

Matches 80; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSGRVTTCASENVVTVYSWTQKPEQSPKLIIVGASNRYTCVDP 60

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1 DIVMTQSTFTNSTVGDRSVTCKASQNGVNTAVYQKPGQSPKALIYSASYPYSGVPH 60

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QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
DB 61 RFTGSGGDTFTLTISNQSEDLABYFCQYNSYPTFGGKLEIK 107

RESULT 2
Q9JL74 PRELIMINARY; PRT; 99 AA.
AC Q9JL74;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Anti-myoisin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206032; AAF69330.1; -.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 10939 MW; 3B25D0E784533324 CRC64;

Query Match 67.3%; Score 378; DB 11; Length 99;
Best Local Similarity 74.7%; Pred. No. 2.5e-33;
Matches 74; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 9 KMSMSVGRVTLTKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPDRFTGSGSA 68
DB 1 KFLVSAAGRVITTCASQSVSNVAMVYQKPGQSPKLLIYGASNRVTGVPDRFTGSGYG 60

QY 69 TDTFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
DB 61 TDTFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 99

RESULT 3
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Anti-myoisin immunoglobulin kappa light chain
DE variable region (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Aderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic arthritis: human anti-N-acetylglucosamine/anti-myoisin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).

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DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4B43E9C5B577F16 CRC64;

Query Match 65.9%; Score 370.5; DB 4; Length 107;
Best Local Similarity 65.4%; Pred. No. 1.8e-32;
Matches 70; Conservative 19; Mismatches 17; Indels 1; Gaps 1;

QY 1 NIWMTQSPKMSMSVGERVTLTKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
DB 1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASLSQGYPS 60

QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
DB 61 RFTGSGGDTFTLTISLQPEDFATYTCQSYSTLTFTGGGKVEIK 106

RESULT 4
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277339; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Barney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; 1REI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 65.7%; Score 369; DB 4; Length 108;
Best Local Similarity 63.6%; Pred. No. 2.7e-32;
Matches 66; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

QY 1 NIWMTQSPKMSMSVGERVTLTKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
DB 1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASLSQGYPS 60

QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGKLEIK 107
DB 61 RFTGSGGDTFTLTISLQPEDFATYTCQSYSTLTFTGGGKVEIK 107

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RESULT 5
Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
DR PIR; D30607; D30607.
DR PIR; D30608; D30608.
DR PIR; F30607; F30607.
DR PIR; F30608; F30608.
DR PIR; G30601; G30601.
DR PIR; G30608; G30608.
DR PIR; H30607; H30607.
DR PIR; H30608; H30608.
DR PIR; I30601; I30601.
DR PIR; I30607; I30607.
DR PIR; I30608; I30608.
DR PIR; PH0963; PH0963.
DR PIR; PH0965; PH0965.
DR PIR; S34096; S34096.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7BE197 CRC64;

Query Match 65.2%; Score 366.5; DB 4; Length 109;
Best Local Similarity 65.4%; Pred. No. 5.1e-32;
Matches 70; Conservative 20; Mismatches 16; Indels 1; Gaps 1;

QY 2 IYVTSQPKSMVSGERVTLTKASENV-VTVSVYQKQKPEQSKLLIYGASNYTGVPD 60
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
2 IYVTSQPGTSLSPGERATLSQASQSVSSYLAWYQKQKPGCAPRLIYGASSRATGIPD 61
QY 61 RFTGSGSATDFTLTSSVOAEDLADYHCGQGYSPYTFGGGKLEIK 107
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
62 RFTSGSGSGTDFLTLSRLPEPCAVYCYQYCGSSPLTFGGGKVEIK 108

RESULT 6
Q9ER29 PRELIMINARY; PRT; 107 AA.
AC Q9ER29;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti human TNF-alpha light chain variable region (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
   human TNF-alpha specific monoclonal antibody."
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the light chain fragment of variable region
   genes of an anti-hTNF-a monoclonal antibody."
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF262753; AAG23804.1; -.
DR PDB; 2AP2; 24-NOV-99.
DR PDB; 43C9; 24-JUL-02.
DR PDB; 43CA; 24-JUL-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 107
FT NON_TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 65.1%; Score 366; DB 11; Length 107;
Best Local Similarity 64.5%; Pred. No. 5.6e-32;
Matches 69; Conservative 17; Mismatches 15; Indels 6; Gaps 1;

QY 4 MTQSPKSMVSGERVTLTKASENV-----TYVSVYQKQKPEQSKLLIYGASNYTG 57
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 MTQSPSSLAMVGGQKVTWMSKSSQSVLNSNTQKNYLAWYQKQKPELIVYFASTREG 60
QY 58 VPDRTGSGSATDFTLTSSVOAEDLADYHCGQGYSPYTFGGGKTL 104
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 VPDRTGSGSGTDFLTLTSSVQTEDLADYFCQHYRTFFFGSGTKL 107
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RESULT 7
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -.
DR PIR; D30609; D30609.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 65.1%; Score 366; DB 11; Length 107;
Best Local Similarity 64.5%; Pred. No. 5.6e-32;
Matches 69; Conservative 17; Mismatches 15; Indels 6; Gaps 1;

QY 4 MTQSPKSMVSGERVTLTKASENV-----TYVSVYQKQKPEQSKLLIYGASNYTG 57
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 MTQSPSSLAMVGGQKVTWMSKSSQSVLNSNTQKNYLAWYQKQKPELIVYFASTREG 60
QY 58 VPDRTGSGSATDFTLTSSVOAEDLADYHCGQGYSPYTFGGGKTL 104
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 VPDRTGSGSGTDFLTLTSSVQTEDLADYFCQHYRTFFFGSGTKL 107
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DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 109
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match
  64.7%; Score 363.5; DB 4; Length 109;
Best Local Similarity 65.4%; Pred. No. 1.1e-31;
Matches 70; Conservative 19; Mismatches 17; Indels 1; Gaps 1;

Qy 2 IVNTQSPKSMMSVGERVTLTKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPDR 61
Db 2 IVNTQSPATLVSFGERATLSCWASISSNLAWYQKPGQAPRLIYGASTRATGIPAR 61

62 FTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

62 FSGSGGTERTLTISLSQSEDFAIYHCQQYNSWPLTFGGGKVEIK 108
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC002035; AA02035.1; -.
DR PIR; A31807; A31807.
DR PIR; A32248; A32248.
DR PIR; B32248; B32248.
DR PIR; C32248; C32248.
DR PIR; F32530; F32530.
DR PIR; PH1042; PH1042.
DR PIR; PH1043; PH1043.
DR PIR; PH1044; PH1044.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S24500; S24500.
DR PIR; S24501; S24501.
DR PIR; S24503; S24503.
DR PIR; S24504; S24504.
DR PIR; S24529; S24529.
DR PIR; S24532; S24532.
DR PIR; S24533; S24533.
DR PIR; S24535; S24535.
DR PIR; S24536; S24536.
DR PIR; S24538; S24538.
DR PIR; I191; I191.
DR PIR; 25-DEC-02.
DR PIR; ILO2; ILO2.
DR PIR; ILO4; ILO4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match
  64.7%; Score 363.5; DB 11; Length 238;
Best Local Similarity 59.8%; Pred. No. 2.9e-31;
Matches 67; Conservative 22; Mismatches 18; Indels 5; Gaps 1;

Qy 1 NIVNTQSPKSMMSVGERVTLTKASENVV-----TVVSWYQKPEQSPKLLIYGASNRY 55
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Db 20 DVVMTQTPLSLPVSIGDQASISCRSSOSIVHSNGNTYLEWYQKPGSPKLLIYKVSNR 79
Qy 56 TGVPRFTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107
Db 80 SGVPRFSGSGGTFTLTISRVEADLGVYFCQGSHPVYTFGGGKLEIK 131

RESULT 9
Q72473 PRELIMINARY; PRT; 234 AA.
AC Q72473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RA Strausberg R.;
RL MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Heide F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Diatchenko L.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Udell T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Raha S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaby S.J.;
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Pahey J.; Helton E.; Kettman M.; Madan A.; Rodrigues S.; Sanchez A.;
RA Whiting M.; Madsen A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
RA Krzywinski M.I.; Skalska U.; Small U.; Schnerch A.; Schein J.E.;
RA Jones S.J.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BC056256; AAH56256.1; -.
DR EMBL; BC056256; AAH56256.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match
  63.7%; Score 358; DB 4; Length 234;
Best Local Similarity 61.3%; Pred. No. 1.1e-30;
Matches 65; Conservative 21; Mismatches 20; Indels 0; Gaps 0;

Qy 2 IVNTQSPKSMMSVGERVTLTKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPDR 61
Db 22 IVNTQSPSFSASTGDRVTIICRASQSIGSYLANWYQKPGKAPQLIYAASLTQSGVPSR 81

62 FTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

62 FSGSGGTERTLTISLSQSEDFATYCCQYTYPTWTFGGGKVEIK 127
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
```

DE Myosin-reactive immunoglobulin light chain variable region
OS (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RZ Wu X., Liu B., van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035035; AAD56271.1; -.
DR FIRM; S23638; S23638.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 63.5%; Score 357; DB 4; Length 108;
Best Local Similarity 60.7%; Pred. No. 5.4e-31;
Matches 65; Conservative 21; Mismatches 21; Indels 0; Gaps 0;

QY 1 NIWMTQSPKSMMSVGERVTLTKASENVVTVVSWYQKPEQSPKLLIYGASNYRTGVPD 60
Db 1 DIWMTQSPSSLSASVGDVTITCRASQDISNYLAWFOQKPKAPKSLIYGASSLQSGVPS 60
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGTKLEIK 107
Db 61 RPSGSGSGTDFLTISLQPEDFATYYCQYKSYPTFGGTKLEIK 107

RESULT 11
Q723Y4 PRELIMINARY; PRT; 236 AA.
AC Q723Y4
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RZ MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Fawcett A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozny K.C., Hale S., Garcia A.M., Gay L.J., Hulyx S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005332; AAH05332.1; -.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBF4ED23084BC6 CRC64;

Query Match 63.5%; Score 357; DB 4; Length 236;
Best Local Similarity 62.6%; Pred. No. 1.5e-30;
Matches 67; Conservative 19; Mismatches 21; Indels 0; Gaps 0;

QY 1 NIWMTQSPKSMMSVGERVTLTKASENVVTVVSWYQKPEQSPKLLIYGASNYRTGVPD 60
Db 23 DIWMTQSPSSLSASVGDVTITCRASQDISNYLAWFOQKPKAPKSLIYGASSLQSGVPS 82
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGTKLEIK 107
Db 83 RPSGSGSGTDFLTISLQPEDFATYYCQYKSYPTFGGTKLEIK 129

RESULT 12
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RZ MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035044; AAD56280.1; -.
DR FIRM; P01607; IREI.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 63.0%; Score 354; DB 4; Length 108;
Best Local Similarity 63.6%; Pred. No. 1.1e-30;
Matches 68; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 NIWMTQSPKSMMSVGERVTLTKASENVVTVVSWYQKPEQSPKLLIYGASNYRTGVPD 60
Db 1 DIWMTQSPSSLSASVGDVTITCRASQDISNYLAWFOQKPKAPKSLIYGASSLQSGVPS 60
QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGTKLEIK 107
Db 61 RPSGSGSGTDFLTISLQPEDVATYYCQKYNAPRTFGGTKLEIK 107

RESULT 13
Q9UL81 PRELIMINARY; PRT; 107 AA.
ID Q9UL81

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 16, 2004, 11:08:07 ; Search time 15.0852 Seconds
(without alignments)
396.986 Million cell updates/sec

Title: US-09-889-300A-1
Perfect score: 614
Sequence: 1 QVQLQQSGAELVRFGTSVKV.....ARDGPWFAYWGQGLTVVSA 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554.5	90.3	119	1	US-08-458-516-11
2	554.5	90.3	138	1	US-08-458-516-7
3	546.5	89.0	119	3	US-08-767-128-10
4	510.5	83.1	138	3	US-08-589-939-1
5	503.5	82.0	119	1	US-08-458-516-10
6	503.5	82.0	222	1	US-08-458-516-22
7	503.5	82.0	235	1	US-08-458-516-23
8	503.5	82.0	449	1	US-08-458-516-13
9	497.5	81.0	117	3	US-09-157-370-2
10	490.5	79.9	119	3	US-08-767-128-20
11	485.5	79.1	121	3	US-08-881-037-65
12	482.5	78.6	119	2	US-08-737-560A-10
13	482	78.5	122	2	US-07-916-098A-10
14	481.5	78.4	119	4	US-09-438-954-39
15	480	78.2	137	1	US-08-392-419-2
16	478.5	77.9	123	1	US-08-497-312-15
17	478.5	77.9	123	2	US-08-560-558E-28
18	478	77.9	120	3	US-08-397-411-11
19	478	77.9	122	1	US-08-236-520-9
20	478	77.9	122	5	PCR-US95-05262-9
21	478	77.9	139	2	US-08-656-586-4
22	477	77.7	116	1	US-07-634-278-3
23	477	77.7	116	1	US-07-634-278-14
24	477	77.7	116	1	US-08-477-728-3
25	477	77.7	116	1	US-08-477-728-14
26	477	77.7	116	1	US-08-474-040-3
27	477	77.7	116	1	US-08-474-040-14

28	477	77.7	116	1	US-08-487-200-3	Sequence 3, Appli
29	477	77.7	116	1	US-08-487-200-14	Sequence 14, Appl
30	477	77.7	116	1	US-08-488-113B-167	Sequence 167, App
31	477	77.7	116	1	US-08-477-484B-167	Sequence 167, App
32	477	77.7	116	1	US-08-107-669D-53	Sequence 53, Appl
33	477	77.7	116	1	US-08-472-788A-85	Sequence 85, Appl
34	477	77.7	116	2	US-08-477-531B-53	Sequence 53, Appl
35	477	77.7	116	2	US-08-646-360-167	Sequence 167, App
36	477	77.7	116	2	US-08-082-842A-85	Sequence 85, Appl
37	477	77.7	116	3	US-08-839-765-167	Sequence 167, App
38	477	77.7	116	3	US-09-136-389-167	Sequence 167, App
39	477	77.7	116	3	US-08-484-537-3	Sequence 3, Appli
40	477	77.7	116	3	US-08-484-537-14	Sequence 14, Appl
41	477	77.7	116	4	US-09-610-838-167	Sequence 167, App
42	477	77.7	116	4	US-09-711-485-167	Sequence 167, App
43	477	77.7	118	2	US-08-428-257A-74	Sequence 74, Appl
44	477	77.7	118	3	US-07-987-264-14	Sequence 14, Appl
45	477	77.7	239	3	US-08-279-772A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-458-516-11
; Sequence 11, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal fragment
US-08-458-516-11

Query Match 90.3%; Score 554.5; DB 1; Length 119;
Best Local Similarity 91.6%; Pred. No. 5.4e-45;
Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;
QY 1 QVQLQQSGAELVRFGTSVKVSKASGYAFTNLIWYKQRPQGLEWIGVNFPGSGTNY 60

Db 1 QVQLQSGAELVPGTISVRVSKASGYAFNLYLIEWVKRPGQGLEWIGVTPGSGGTNY 60
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCA-RDG--PWFAYWGQGLTVTVSA 116
Db 61 NEKFKGKATLTVDKSSITAYMQLSSLTSDSAVYFCARRDGNYGWFAYWGRGLTVTVSA 119

RESULT 2

US-08-458-516-7
; Sequence 7, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIb/IIIa
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/059,159

FILING DATE: 03-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-37-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 138 amino acids

TYPE: amino acid

MOLECULE TYPE: linear

US-08-458-516-7

Query Match

Best Local Similarity 90.3%; Score 554.5; DB 1; Length 138;

Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

QY 1 QVQLQSGAELVPGTISVRVSKASGYAFNLYLIEWVKRPGQGLEWIGVTPGSGGTNY 60

Db 20 QVQLQSGAELVPGTISVRVSKASGYAFNLYLIEWVKRPGQGLEWIGVTPGSGGTNY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCA-RDG--PWFAYWGQGLTVTVSA 116

Db 80 NEKFKGKATLTVDKSSITAYMQLSSLTSDSAVYFCARRDGNYGWFAYWGRGLTVTVSA 138

RESULT 3

US-08-767-128-10

; Sequence 10, Application US/08767128

; Patent No. 6111079

; GENERAL INFORMATION:

; APPLICANT: WYLIE, DWANE E.

; APPLICANT: LOPEZ, OSVALDO

; APPLICANT: MURRAY, PETER JOSEPH

; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/767,128

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/09258

FILING DATE: 05-JUN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 04-DEC-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/09258

FILING DATE: 05-JUN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/541,373

FILING DATE: 10-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/462,798

FILING DATE: 05-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Carter, Charles G.

REGISTRATION NUMBER: 35,093

REFERENCE/DOCKET NUMBER: 8648.49USF1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612/371-5278

TELEFAX: 612/332-9081

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

US-08-767-128-10

Query Match

Best Local Similarity 89.0%; Score 546.5; DB 3; Length 119;

Matches 107; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVPGTISVRVSKASGYAFNLYLIEWVKRPGQGLEWIGVTPGSGGTNY 60

Db 1 EVQLQSGAELVPGTISVRVSKASGYAFNLYLIEWVKRPGQGLEWIGVTPGSGGTNY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGP---WYAYWGQGLTVTVSA 116

Db 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARSGYGHWYFDVWGAGTTTVSS 119

RESULT 4

US-08-589-939-1

; Sequence 1, Application US/08589939

; Patent No. 6015662

; GENERAL INFORMATION:

; APPLICANT: Hackett, Jr., John R.

```
;
; APPLICANT: Hoff, Jane A.
; APPLICANT: Ostrow, David H.
; APPLICANT: Golden, Alan M.
; TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND
; TITLE OF INVENTION: CONTROLS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,939
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5865.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-589-939-1

Query Match      83.1%; Score 510.5; DB 3; Length 138;
Best Local Similarity 84.9%; Pred. NO. 8.5e-41;
Matches 101; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY      1 QVQLQSGAEIVRGTSVKVSKASGYAFTNLYLIEWKQRPQGQLEWIGVINPGSGGTNY 60
Db      20 QVHLQSGAEIVRGTSVKVSKASGYAFTNLYLIEWKQRPQGQLEWIGVINPGSDFTYY 79
QY      61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCAR---DGPWFAYWGQGLTVTVSA 116
Db      80 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARTIVTDYFDWGGQGLTVTVSS 138

RESULT 5
US-08-458-516-10
; Sequence 10, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 22:
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal fragment
; US-08-458-516-10

Query Match      82.0%; Score 503.5; DB 1; Length 119;
Best Local Similarity 80.7%; Pred. NO. 3.3e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

QY      1 QVQLQSGAEIVRGTSVKVSKASGYAFTNLYLIEWKQRPQGQLEWIGVINPGSGGTNY 60
Db      1 QVQLVQSGAEIVKFGSSVKVSKASGYAFTNLYLIEWVRQAPGQGLEWIGVYFSGGTNY 60
QY      61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCA-RDG--PWFAYWGQGLTVTVSA 116
Db      61 NEKFKGRVTLTVDSTNTAYMELSLRSEDVAVYFCARRDGNVGFAYWGQGLTVTVSS 119

RESULT 6
US-08-458-516-22
; Sequence 22, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 22:
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SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-22

Query Match 82.0%; Score 503.5; DB 1; Length 222;
Best Local Similarity 80.7%; Pred. No. 6.4e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

Qy 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGYAFTNLYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60

Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCA-RDG--PWFAYWGQGLTIVTSA 116
Db 61 NEKFKGRVTLTVDESTINTAYMELSLRSEDATVYFCARRDGNYGWFAIWGQGLTIVTSS 119

RESULT 7

US-08-458-516-23
Sequence 23, Application US/08458516
Patent No. 5777085

GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-23

Query Match 82.0%; Score 503.5; DB 1; Length 235;
Best Local Similarity 80.7%; Pred. No. 6.8e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

Qy 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGYAFTNLYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60

Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCA-RDG--PWFAYWGQGLTIVTSA 116
Db 61 NEKFKGRVTLTVDESTINTAYMELSLRSEDATVYFCARRDGNYGWFAIWGQGLTIVTSS 119

RESULT 8

US-08-458-516-13
Sequence 13, Application US/08458516
Patent No. 5777085

GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-13

Query Match 82.0%; Score 503.5; DB 1; Length 449;
Best Local Similarity 80.7%; Pred. No. 1.4e-39;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

Qy 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGYAFTNLYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60

Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCA-RDG--PWFAYWGQGLTIVTSA 116
Db 61 NEKFKGRVTLTVDESTINTAYMELSLRSEDATVYFCARRDGNYGWFAIWGQGLTIVTSS 119

RESULT 9

US-09-157-370-2
Sequence 2, Application US/09157370A
Patent No. 6262238

GENERAL INFORMATION:
APPLICANT: STEIPE, Boris
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
FILE REFERENCE: P8341-8072

;; CURRENT APPLICATION NUMBER: US/09/157,370A
;; CURRENT FILING DATE: 1998-09-21
;; EARLIER APPLICATION NUMBER: 08/765,179
;; EARLIER FILING DATE: 1997-01-14
;; EARLIER APPLICATION NUMBER: PCT/EP95/02626
;; EARLIER FILING DATE: 1995-07-06
;; EARLIER APPLICATION NUMBER: DE/P44 25 115.7
;; EARLIER FILING DATE: 1994-07-15
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 117
;; TYPE: PRT
;; ORGANISM: Mus sp.
US-09-157-370-2

Query Match 81.0%; Score 497.5; DB 3; Length 117;
Best Local Similarity 80.3%; Pred. No. 1.2e-39;
Matches 94; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
QY 1 OVLOQSGAEIVRPGTSVKVSKASGYAFTNYLIEWVKQPGGGLWIGVINPGSGGTNY 60
Db 1 EVLOQSGGELVPGASVKLSKASGYFTSYNHWVKQRPKGLEWIGRINFGSGGTNY 60
QY 61 NEKFKGKATLTADKSSSTAYMQLSLSLTDSDSNAVYFCARDG-PWFAYWGQGTTLVTSA 116
Db 61 NEKFKGKATLTADKSSSTAYMQLSLSLTDSDSNAVYFCARDG-PWFAYWGQGTTLVTSS 117

RESULT 10
US-08-767-128-20
; Sequence 20, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093

;; REFERENCE/DOCKET NUMBER: 8648.49USFI
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612/371-5278
;; TELEFAX: 612/332-9081
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;; ORIGINAL SOURCE:
US-08-767-128-20
Query Match 79.9%; Score 490.5; DB 3; Length 119;
Best Local Similarity 78.2%; Pred. No. 5.4e-39;
Matches 93; Conservative 10; Mismatches 13; Indels 3; Gaps 1;
QY 1 OVLOQSGAEIVRPGTSVKVSKASGYAFTNYLIEWVKQPGGGLWIGVINPGSGGTNY 60
Db 1 QVLOQSGVELMKFGASVKISCKATGYTFSSYIEWVKQRPKGLEWIGLEILPGSGGTNY 60
QY 61 NEKFKGKATLTADKSSSTAYMQLSLSLTDSDSNAVYFCAR---DGFWYWGQGTTLVTSA 116
Db 61 NEKFKGKATLTADTSSNTAYMQVSSLTSDSNAVYFCARIYYGHLWYWGQGTTLVTSA 119
RESULT 11
US-08-881-037-65
; Sequence 65, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: GLICK, GARY D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Koneki, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
US-08-881-037-65

Query Match          79.1%; Score 485.5; DB 3; Length 121;
Best Local Similarity 80.0%; Pred. No. 1.6e-38;
Matches 96; Conservative 4; Mismatches 15; Indels 5; Gaps 1;

Qy 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNYLIEWVKORPGQGLEWIGVINPGSGGTNY 60
Db 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNYLIEWVKORPGQGLEWIGVINPGSGGTNY 60

Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDG-----PWFAYWGQGLTVTVS 115
Db 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDG-----PWFAYWGQGLTVTVS 120

RESULT 12
US-08-737-560A-10
; Sequence 10, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuul
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuul
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: 4B4-1-1 heavy chain variable region
US-08-737-560A-10

Query Match          78.6%; Score 482.5; DB 2; Length 119;
Best Local Similarity 79.0%; Pred. No. 3e-38;
Matches 94; Conservative 8; Mismatches 14; Indels 3; Gaps 1;

; TOPOLOGY: linear
US-07-916-098A-10

Query Match          78.5%; Score 482; DB 2; Length 122;
Best Local Similarity 72.1%; Pred. No. 3.5e-38;
Matches 88; Conservative 19; Mismatches 9; Indels 6; Gaps 1;

Qy 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNYLIEWVKORPGQGLEWIGVINPGSGGTNY 60
Db 1 EVKLQESGPELVKFOASVKMSCKASGYFTTSYIHWVRQPGGGLDWIGVINPDGTDY 60

Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARD-----GPFAYWGQGLTVTV 114
Db 61 DEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCAREKDNVATGAWFAYWGQGLTVTV 120
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QY 115 SA 116
Db 121 SS 122

RESULT 14

US-09-438-954-39
; Sequence 39, Application US/09438954
; Patent No. 6458934
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-LBB AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING SAME
; FILE REFERENCE: 1303-124P
; CURRENT APPLICATION NUMBER: US/09/438,954
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Variable
; OTHER INFORMATION: region of heavy chain of mouse monoclonal antibody
; OTHER INFORMATION: 434-1-1
US-09-438-954-39

Query Match 78.4%; Score 481.5; DB 4; Length 119;
Best Local Similarity 79.0%; Pred. No. 3.8e-35;
Matches 94; Conservative 8; Mismatches 14; Indels 3; Gaps 1;
QY 1 QVQLQQSGAELVRPGTSVKVSKASGVAFTNLYLIEWVKQRPQGCGLEWIGVINPGSGGTNY 60
Db 1 QVQLQQSGAELVRPGTSVKVSKASGVAFTNLYLIEWVKQRPQGCGLEWIGVINPGSGGTNY 60
QY 61 NEKPKGKATLTADKSSSTAYMQLSSLTSDSVAVYFCARD--GPWFAYWGQGLTIVTUSA 116
Db 61 NEKPKSKATLTVDKSSSTAYMQLSSLTSDSVAVYCARSTTARAFAYWGQGLTIVTUSA 119

RESULT 15

US-08-392-419-2
; Sequence 2, Application US/08392419
; Patent No. 5624659
; GENERAL INFORMATION:
; APPLICANT: Bigner, Darrell D.
; APPLICANT: Zalutsky, Michael R.
; TITLE OF INVENTION: METHOD OF TREATMENT
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 5624659th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,419
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/033,827
; FILING DATE: 19-MAR-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5405-90
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-392-419-2
Query Match 78.2%; Score 480; DB 1; Length 137;
Best Local Similarity 77.1%; Pred. No. 6.1e-38;
Matches 91; Conservative 12; Mismatches 13; Indels 2; Gaps 1;
QY 1 QVQLQQSGAELVRPGTSVKVSKASGVAFTNLYLIEWVKQRPQGCGLEWIGVINPGSGGTNY 60
Db 20 EVQLQQSGPELVKPGASVKMSCKASGYTFISYVHVHVKQNPFGCGLEWIGVINPFNDGTKY 79
QY 61 NEKPKGKATLTADKSSSTAYMQLSSLTSDSVAVYFCARD--GPWFAYWGQGLTIVTUSA 116
Db 80 NEKPKSKATLTSDRSSSTAYMQLSSLTSESAVYFCARDMGREGFAYWGQGLTIVTUSA 137
Search completed: August 16, 2004, 11:12:57
Job time : 16.0852 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 16, 2004, 11:10:36 ; Search time 42.1345 seconds
(without alignments)
864.269 Million cell updates/sec

Title: US-09-889-300A-1

Perfect score: 614

Sequence: 1 QVQLQQSGAEIVRGTSTVKV.....ARDGPWFAYWGQTLVTGSA 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications RA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554.5	90.3	119	12	US-10-411-037-54 Sequence 54, Appl
2	554.5	90.3	119	12	US-10-411-026-54 Sequence 54, Appl
3	554.5	90.3	119	16	US-10-410-962-54 Sequence 54, Appl
4	554.5	90.3	119	16	US-10-411-049-54 Sequence 54, Appl
5	554.5	90.3	119	16	US-10-410-930-54 Sequence 54, Appl
6	554.5	90.3	119	16	US-10-410-997-54 Sequence 54, Appl
7	554.5	90.3	119	16	US-10-411-012-54 Sequence 54, Appl
8	554.5	90.3	119	16	US-10-287-994-54 Sequence 54, Appl
9	554.5	90.3	119	16	US-10-410-913-54 Sequence 54, Appl
10	519	84.5	138	13	US-10-146-305-8 Sequence 8, Appl
11	503.5	82.0	119	12	US-10-411-037-53 Sequence 53, Appl
12	503.5	82.0	119	12	US-10-411-026-53 Sequence 53, Appl
13	503.5	82.0	119	16	US-10-410-962-53 Sequence 53, Appl
14	503.5	82.0	119	16	US-10-411-049-53 Sequence 53, Appl
15	503.5	82.0	119	16	US-10-410-930-53 Sequence 53, Appl

16	503.5	82.0	119	16	US-10-410-997-53 Sequence 53, Appl
17	503.5	82.0	119	16	US-10-411-012-53 Sequence 53, Appl
18	503.5	82.0	119	16	US-10-287-994-53 Sequence 53, Appl
19	503.5	82.0	119	16	US-10-410-913-53 Sequence 53, Appl
20	503.5	82.0	448	12	US-10-411-037-56 Sequence 56, Appl
21	503.5	82.0	448	12	US-10-411-026-56 Sequence 56, Appl
22	503.5	82.0	448	16	US-10-410-962-56 Sequence 56, Appl
23	503.5	82.0	448	16	US-10-411-049-56 Sequence 56, Appl
24	503.5	82.0	448	16	US-10-410-930-56 Sequence 56, Appl
25	503.5	82.0	448	16	US-10-410-997-56 Sequence 56, Appl
26	503.5	82.0	448	16	US-10-411-012-56 Sequence 56, Appl
27	503.5	82.0	448	16	US-10-287-994-56 Sequence 56, Appl
28	503.5	82.0	448	16	US-10-410-913-56 Sequence 11, Appl
29	490.5	79.9	113	16	US-10-307-276B-11 Sequence 11, Appl
30	489	79.6	139	13	US-10-006-773-13 Sequence 11, Appl
31	488	79.5	118	15	US-10-435-614-11 Sequence 20, Appl
32	488	79.5	260	15	US-10-435-614-20 Sequence 21, Appl
33	486	79.2	118	15	US-10-435-614-13 Sequence 13, Appl
34	486	79.2	177	15	US-10-435-614-21 Sequence 5, Appl
35	485.5	79.1	113	16	US-10-307-276B-5 Sequence 7, Appl
36	485.5	79.1	113	16	US-10-307-276B-7 Sequence 2, Appl
37	485.5	79.1	117	15	US-10-447-257-2 Sequence 66, Appl
38	485.5	79.1	143	14	US-10-010-729-66 Sequence 2, Appl
39	485	79.0	118	16	US-10-467-546-2 Sequence 4, Appl
40	485	79.0	448	16	US-10-467-546-4 Sequence 2, Appl
41	483.5	78.7	119	12	US-10-153-024-2 Sequence 6, Appl
42	483	78.7	195	14	US-10-360-053-6 Sequence 8, Appl
43	483	78.7	195	14	US-10-360-053-8 Sequence 3, Appl
44	482.5	78.6	113	16	US-10-307-276B-3 Sequence 5, Appl
45	482.5	78.6	119	12	US-10-460-595-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-10-411-037-54
; Sequence 54, Application US/10411037
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-037-54

Query Match	90.3%	Score 554.5	DB 12	Length 119
Best Local Similarity	91.6%	Pred. No. 1.8e-45		
Matches 109	Conservative 3	Mismatches 4	Indels 3	Gaps 2

QY	1	QVQLQSGAEILVRPGTSVKVSKASGYAFTNYLIEWKORPGGLEWIGVINPGSGGTNY	60
Db	1	QVQLQSGAEILVRPGTSVRVSKASGYAFTNYLIEWKORPGGLEWIGVIYVPGSGGTNY	60

QY	61	NEKFKGKATLTADKSSSTAYNQQLSSLTSDSSAVYFCA-RDG--PWFAYWGQGLTLVTVSA	116
Db	61	NEKFKGKATLTVDKSSITAYNQQLSSLTSDSSAVYFCARRDGNYGWFAYWGRGTLVTVSA	119

RESULT 2

US-10-411-026-54

Sequence 54, Application US/10411026

Publication No. US20040063911A1

GENERAL INFORMATION:

APPLICANT: Neose Technologies, Inc.

APPLICANT: Defrees, Shawn

APPLICANT: Zopf, David

APPLICANT: Bayer, Robert

APPLICANT: Hakes, David

APPLICANT: Chen, Xi

TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED THEREFROM

TITLE OF INVENTION: METHODS

FILE REFERENCE: 040853-01-5053

CURRENT APPLICATION NUMBER: US/10/411,026

PRIOR FILING DATE: 2003-04-09

PRIOR APPLICATION NUMBER: US 60/328,523

PRIOR FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR FILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: US 60/404,249

PRIOR FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR FILING DATE: 2002-08-28

NUMBER OF SEQ ID NOS: 75

SOFTWARE: PatentIn version 3.2

SEQ ID NO 54

LENGTH: 119

TYPE: PRT

ORGANISM: Mus musculus

US-10-411-026-54

Query Match	90.3%	Score 554.5	DB 12	Length 119
Best Local Similarity	91.6%	Pred. No. 1.8e-45		
Matches 109	Conservative 3	Mismatches 4	Indels 3	Gaps 2

QY	1	QVQLQSGAEILVRPGTSVKVSKASGYAFTNYLIEWKORPGGLEWIGVINPGSGGTNY	60
Db	1	QVQLQSGAEILVRPGTSVRVSKASGYAFTNYLIEWKORPGGLEWIGVIYVPGSGGTNY	60

QY	61	NEKFKGKATLTADKSSSTAYNQQLSSLTSDSSAVYFCA-RDG--PWFAYWGQGLTLVTVSA	116
Db	61	NEKFKGKATLTVDKSSITAYNQQLSSLTSDSSAVYFCARRDGNYGWFAYWGRGTLVTVSA	119

RESULT 3

US-10-410-962-54

Sequence 54, Application US/10410962

Publication No. US2004007836A1

GENERAL INFORMATION:

APPLICANT: Neose Technologies, Inc.

APPLICANT: Defrees, Shawn

APPLICANT: Zopf, David

; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-049-54

Query Match 90.3%; Score 554.5; DB 16; Length 119;
Best Local Similarity 91.6%; Pred. No. 1.8e-45;
Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

QY 1 QVQLQSGAELVRPGTSVKVSKAGSYFTNYLIEWKQRPQGQLEWGVINPGSGGTNY 60
Db 1 QVQLQSGAELVRPGTSVRVSKAGSYFTNYLIEWKQRPQGQLEWGVINPGSGGTNY 60
QY 61 NEKFKGKATLTADKSSSTAYVQLSLLTSDSAVYFCA-RDG--PWFAYWGQGLTVTSA 116
Db 61 NEKFKGKATLTVDKSTTAYVQLSLLTSDSAVYFCARRDGNYGWFAYWGRGLTVTSA 119

RESULT 5

US-10-410-930-54
; Sequence 54, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE OF INVENTION: BETA
; FILE REFERENCE: 040853-01-5056
; CURRENT APPLICATION NUMBER: US/10/410,930
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-410-930-54

Query Match 90.3%; Score 554.5; DB 16; Length 119;
Best Local Similarity 91.6%; Pred. No. 1.8e-45;
Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;
QY 1 QVQLQSGAELVRPGTSVKVSKAGSYFTNYLIEWKQRPQGQLEWGVINPGSGGTNY 60
Db 1 QVQLQSGAELVRPGTSVRVSKAGSYFTNYLIEWKQRPQGQLEWGVINPGSGGTNY 60
QY 61 NEKFKGKATLTADKSSSTAYVQLSLLTSDSAVYFCA-RDG--PWFAYWGQGLTVTSA 116
Db 61 NEKFKGKATLTVDKSTTAYVQLSLLTSDSAVYFCARRDGNYGWFAYWGRGLTVTSA 119

RESULT 6

US-10-410-997-54
; Sequence 54, Application US/10410997
; Publication No. US20040126838A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
; FILE OF INVENTION: FSH
; FILE REFERENCE: 040853-01-5059
; CURRENT APPLICATION NUMBER: US/10/410,997
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-410-997-54

Query Match 90.3%; Score 554.5; DB 16; Length 119;
Best Local Similarity 91.6%; Pred. No. 1.8e-45;
Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;
QY 1 QVQLQSGAELVRPGTSVKVSKAGSYFTNYLIEWKQRPQGQLEWGVINPGSGGTNY 60
Db 1 QVQLQSGAELVRPGTSVRVSKAGSYFTNYLIEWKQRPQGQLEWGVINPGSGGTNY 60
QY 61 NEKFKGKATLTADKSSSTAYVQLSLLTSDSAVYFCA-RDG--PWFAYWGQGLTVTSA 116
Db 61 NEKFKGKATLTVDKSTTAYVQLSLLTSDSAVYFCARRDGNYGWFAYWGRGLTVTSA 119

RESULT 7

US-10-411-012-54
; Sequence 54, Application US/10411012
; Publication No. US20040132640A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: GLYCOPOLYMERIZATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5051
; CURRENT APPLICATION NUMBER: US/10/411,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10


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; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-146-305-8

Query Match      84.5%; Score 519; DB 13; Length 138;
Best Local Similarity 83.6%; Pred. No. 5.3e-42;
Matches 102; Conservative 5; Mismatches 9; Indels 6; Gaps 1;

QY 1 QVQLQSGAEIVRPETSVKVKSCASGYAFNTNLYIEWVKRPGQGLEWIGVINPGSGGTNY 60
DB 1 QVQLQSGTEVMVRPGTSVKVKSCASGYPTNHLIEWVKRPGQGPWIGVINPGSGGTNY 60
QY 61 NEKPKGKATLTADKSSSTAYMQLSLTSDSAYVFCA-----RDGPWFAYWGQGLTVTV 114
DB 61 NEKPKGKATLTADKSSSTAYMQLSLTSDSAYVFCAIMTTFLGEGYAMDYWGQGSITV 120
QY 115 SA 116
DB 121 SS 122

RESULT 11
US-10-411-037-53
; Sequence 53, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bows, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/50/411,037
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-53

Query Match      82.0%; Score 503.5; DB 12; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.4e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

QY 1 QVQLQSGAEIVRPETSVKVKSCASGYAFNTNLYIEWVKRPGQGLEWIGVINPGSGGTNY 60
DB 1 QVQLVQSGAEIVKPGSSVKVKSCASGYAFNTNLYIEWVRQAPGQGLEWIGVIYFGSGGTNY 60
QY 61 NEKPKGKATLTADKSSSTAYMQLSLTSDSAYVFCA-RDG--PWFAYWGQGLTVTVA 116
DB 61 NEKPKGRVTLTVDESTNTAYMELSSLSSEDTAVYFCAARRDGNYGWTFAYWGQGLTVTVSS 119

RESULT 12
US-10-411-026-53
; Sequence 53, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bows, Caryn
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-53

Query Match      82.0%; Score 503.5; DB 12; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.4e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

QY 1 QVQLQSGAEIVRPETSVKVKSCASGYAFNTNLYIEWVKRPGQGLEWIGVINPGSGGTNY 60
DB 1 QVQLVQSGAEIVKPGSSVKVKSCASGYAFNTNLYIEWVRQAPGQGLEWIGVIYFGSGGTNY 60
QY 61 NEKPKGKATLTADKSSSTAYMQLSLTSDSAYVFCA-RDG--PWFAYWGQGLTVTVA 116
DB 61 NEKPKGRVTLTVDESTNTAYMELSSLSSEDTAVYFCAARRDGNYGWTFAYWGQGLTVTVSS 119

RESULT 13
US-10-410-962-53
; Sequence 53, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bows, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
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; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 53
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-53
```

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Query Match      82.0%; Score 503.5; DB 16; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.4e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

Qy 1 QVQLQSGAELVRPQTSVKVSKASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60
Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCA-RDG--PWFAYWGQGLTVTVSA 116
Db 61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAWYWGQGLTVTVSS 119
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RESULT 14
US-10-411-049-53
; Sequence 53, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 53
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-411-049-53

Query Match      82.0%; Score 503.5; DB 16; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.4e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

Qy 1 QVQLQSGAELVRPQTSVKVSKASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60
Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCA-RDG--PWFAYWGQGLTVTVSA 116
Db 61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAWYWGQGLTVTVSS 119

RESULT 15
US-10-410-930-53
; Sequence 53, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5056
; CURRENT APPLICATION NUMBER: US/10/410,930
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 53
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-930-53
```

```
Query Match      82.0%; Score 503.5; DB 16; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.4e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

Qy 1 QVQLQSGAELVRPQTSVKVSKASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60
Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCA-RDG--PWFAYWGQGLTVTVSA 116
Db 61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAWYWGQGLTVTVSS 119
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Search completed: August 16, 2004, 11:21:19
Job time : 43.1345 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 16, 2004, 11:08:06 ; Search time 12.4843 Seconds
(without alignments)
893.780 Million cell updates/sec

Title: US-09-889-300A-1
Perfect score: 614
Sequence: 1 QVQLQSGAEIVRGTSVKV.....ARDGPWFAYWGQGLTVTVSA 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	535.5	87.2	123	2 B30560	Ig heavy chain V r
2	526	85.7	123	2 S60067	Ig heavy chain V r
3	491.5	80.0	119	2 S20640	Ig heavy chain V r
4	491	80.0	135	2 A30577	Ig heavy chain pre
5	487.5	79.4	117	2 JC2269	PL7-6 antibody hea
6	487.5	79.4	119	2 C30562	Ig heavy chain V r
7	487	79.3	474	1 G2MS11	Ig gamma-2b chain
8	485	79.0	137	2 F29380	Ig heavy chain pre
9	484	78.8	118	2 C30560	Ig heavy chain V r
10	483.5	78.7	118	2 S38565	Ig heavy chain V r
11	483.5	78.7	138	2 S21810	Ig heavy chain V r
12	482.5	78.6	246	2 S38950	Ig gamma chain - m
13	482.5	78.6	446	2 S40295	Ig gamma-2a chain
14	481.5	78.4	119	2 E30562	Ig heavy chain V r
15	481	78.3	141	2 JL0076	Ig heavy chain pre
16	478.5	77.9	119	2 D30562	Ig heavy chain V r
17	478	77.9	137	2 E29380	Ig heavy chain pre
18	477.5	77.8	131	2 A27472	Ig heavy chain pre
19	476	77.5	140	2 S09216	Ig heavy chain pre
20	475.5	77.4	138	1 HYMS17	Ig heavy chain pre
21	475	77.4	115	2 A54378	Ig heavy chain V r
22	473.5	77.1	140	2 PH1482	Ig heavy chain V r
23	472.5	77.0	118	2 PF0231	Ig heavy chain V r
24	470	76.5	119	2 A24672	Ig heavy chain pre
25	469.5	76.5	117	2 S19966	Ig heavy chain V r
26	469.5	76.5	140	1 HYMS67	Ig heavy chain pre
27	468	76.2	116	2 S09962	Ig heavy chain V-D
28	468	76.2	116	2 S53751	antibody Fab Jel 1
29	467.5	76.1	123	2 E48677	Ig heavy chain V-D

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30 466 75.9 112 2 A30502 Ig heavy chain V r
31 466 75.9 117 2 S25176 Ig heavy chain V r
32 466 75.9 139 1 MHMS18 Ig heavy chain pre
33 466 75.9 141 2 A39276 Ig heavy chain pre
34 466 75.9 287 4 PC4402 pElB leader/Ig hea
35 465.5 75.8 112 2 PL0232 Ig heavy chain V r
36 465.5 75.8 121 2 S19969 Ig heavy chain V r
37 465 75.7 118 2 S38717 Ig heavy chain V r
38 465 75.7 120 2 B22769 Ig heavy chain V r
39 464 75.6 131 2 S66537 Ig heavy chain V r
40 463.5 75.5 123 2 F48677 Ig heavy chain V-D
41 463.5 75.5 138 2 B32513 Ig heavy chain pre
42 462.5 75.3 115 2 A56700 Ig heavy chain (an
43 462.5 75.3 116 2 S55542 Ig heavy chain V r
44 460 74.9 118 2 S37201 Ig heavy chain V r
45 460 74.9 120 2 G28195 Ig heavy chain V r

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ALIGNMENTS

RESULT 1

B30560
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C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 23-Jul-1999
C:Accession: B30560
R: Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A:Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclon.
A:Reference number: A30560; MUID:89110062; PMID:2464028
A:Accession: B30560
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <MAT>
A:Cross-references: GB:M24269; NID:G195619; PIDN:AAA38373.1; PID:G195620
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

```

Query Match      87.2%; Score 535.5; DB 2; Length 123;
Best Local Similarity 87.8%; Pred. No. 1.5e-41;
Matches 108; Conservative 1; Mismatches 7; Indels 7; Gaps 2;

QY 1 QVQLQSGAEIVRGTSVKVSKASGYAFNYLIEWKQPPGGQLEWIGVINFGSGGTNY 60
   |||||
Db 1 QVQLQSGAEIVRGTSVKVSKASGYAFNYLIEWKQRLGQDLEWIGVINFGSGGTNY 60
   |||||
QY 61 NEKPKGRATLTADKSSSTAYWQLSSLTSDSAVYFCAR-----DGPW-FAYWGQGLTVT 113
   |||||
Db 61 NEKPKGRATLTADKSSSTAYWQLSSLTSDSAVYFCARSSPYDYGWYFDVWGAGTTVT 120
   |||||
QY 114 VSA 116
   |||
Db 121 VSS 123

```

RESULT 2

S60067
Ig heavy chain V region (monoclonal antibody C3, gamma 2A) [validated] - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1996 #sequence_revision 10-Oct-1997 #text_change 23-Mar-2001
C:Accession: S60067
R:Wien, M.W.; Filman, D.J.; Stura, E.A.; Guillot, S.; Delpeyroux, F.; Crainic, R.; Hogl-
Net Struct. Biol. 2, 232-243, 1995
A:Title: Structure of the complex between the Fab fragment of a neutralizing antibody fr
A:Reference number: S60066; MUID:95292109; PMID:7539711
A:Accession: S60067
A:Molecule type: mRNA
A:Residues: 1-123 <WIE>
A:Cross-references: EMBL:X84698; NID:G773225
R:Wien, M.W.; Hogle, J.M.

submitted to the Brookhaven Protein Data Bank, January 1995

A;Reference number: A52979; PDB:1FPT
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 1-123
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin; pyroglutamic acid
F;15-98/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;22-96/Disulfide bonds: #status experimental

Query Match 85.7%; Score 526; DB 2; Length 123;
Best Local Similarity 85.0%; Pred. No. 1.1e-40;
Matches 102; Conservative 5; Mismatches 9; Indels 4; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
DB 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLQWIKRPGQGLEWIGVINPGSGGTNY 60
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD---GPWFAYWGQGLTVTSA 116
DB 61 NAFPKGKATLTADKSSSIYVMQLSSLTSDSAVYFCARDFYDYGDFYWGQGLTVTSS 120

RESULT 3

S20640

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C;Accession: S20640; S20644

R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.

submitted to the EMBL Data Library, February 1992

A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react

A;Reference number: S20639

A;Accession: S20640

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-119 <LOS>

A;Cross-references: EMBL:X65002; NID:G52600; PID:CAA46135.1; PID:G52601; EMBL:X64999; N

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 491.5; DB 2; Length 119;
Best Local Similarity 77.3%; Pred. No. 1.4e-37;
Matches 92; Conservative 13; Mismatches 11; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
DB 1 EVQLQSGAELVRPGTSVKVSKASGYAFTNLYLHWVKRPGQGLEWIGVINPYNDGSKY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR---DGPWFAYWGQGLTVTSA 116
DB 61 NEMFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARATKGSWFAWYWGQGLTVTSA 119

RESULT 4

A30577

Ig heavy chain precursor V region (MRL10) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996

C;Accession: A30577

R;Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theof

J. Exp. Med. 161, 805-815, 1985

A;Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely rela

A;Reference number: A30577; MUID:95159423; PMID:3920343

A;Accession: A30577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-135 <KOF>

A;Cross-references: GB:M37621

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 491; DB 2; Length 135;
Best Local Similarity 82.8%; Pred. No. 1.7e-37;
Matches 96; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
DB 20 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLHWVKRPGQGLEWIGVINPGSGGTNY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPWFAYWGQGLTVTSA 116
DB 80 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARLVGGFAYWGQGLTVTSA 135

RESULT 5

JC2269

PL7-6 antibody heavy chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 07-May-1999

C;Accession: JC2269; PC2186

R;Kurose, T.; Katayama, M.; Murakami, K.; Hashino, K.; Kamihagi, K.; Yasumoto, M.; Ka

J. Biochem. 115, 608-614, 1994

A;Title: Expression of recombinant mouse/human chimeric antibody specific to human GM

A;Reference number: JC2269; MUID:94334310; PMID:7520038

A;Accession: JC2269

A;Molecule type: mRNA

A;Residues: 1-117 <KUR>

A;Accession: PC2186

A;Molecule type: protein

A;Residues: 2-27 <KU2>

A;Experimental source: hybridoma cell

C;Comment: This protein is specific to human P-selectin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;2-98/Region: V segment

F;15-98/Domain: immunoglobulin homology <IMM>

F;99-106/Region: D segment

F;107-117/Region: J segment

Query Match 79.4%; Score 487.5; DB 2; Length 117;
Best Local Similarity 78.6%; Pred. No. 3.1e-37;
Matches 92; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
DB 1 EVQLQSGAELVRPGTSVKVSKASGYAFTNLYLHWVKRPGQGLEWIGVINPGTAYTEH 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGP-WFAYWGQGLTVTSA 116
DB 61 NQKFKDKATLTADKSSSTAYMQLSSLTSDSAVYFCASGNPAMPAYWGQGLTVTSA 117

RESULT 6

C30562

Ig heavy chain V region (27.7.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996

C;Accession: C30562

R;Skidder, S.K.; Borden, P.; Gruszo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison,

J. Immunol. 142, 888-893, 1989

A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen

A;Reference number: A30562; MUID:89110066; PMID:2464031

A;Accession: C30562

A;Status: preliminary

A;Residues: 1-119 <SLK>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 487.5; DB 2; Length 119;
Best Local Similarity 79.0%; Pred. No. 3.1e-37;
Matches 94; Conservative 9; Mismatches 13; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKRPGQGLEWIGVINPGSGGTNY 60

Query Match 78.8%; Score 484; DB 2; Length 118;
Best Local Similarity 78.0%; Pred. No. 6.4e-37;
Matches 92; Conservative 10; Mismatches 14; Indels 2; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNYLIEWKQRPQGQLEWIGVINPGSGGTNY 60
DB 1 QVHLQSGAELVRPGASVKISCKASGYTFTSYMMNWVKQRPQGQLEWIGVIDPNSVTNN 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCAR--DGPWFAYWGQTLTVTSA 116
DB 61 NQRFKATLTVDKSSNTAYMQLSLTSDSAVYFCARWGTSWFPAYWGQTLTVTSA 118

RESULT 10
S38565
Ig heavy chain V region (ASWV1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38565
R:Monestier, M.; Logman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A:Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s Y
A:Reference number: S38559
A:Accession: S38565
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <NON>
A:Cross-references: EMBL:X75100; NID:g414157; PIDN:CAA52991.1; PID:g414158
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 483.5; DB 2; Length 118;
Best Local Similarity 78.8%; Pred. No. 7.1e-37;
Matches 93; Conservative 9; Mismatches 13; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNYLIEWKQRPQGQLEWIGVINPGSGGTNY 60
DB 1 EVQLQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPQGQLEWIGVINPGNGTKY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDGP---WFAYWGQTLTVTS 115
DB 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCAREGAGSYFDYWGQTLTVTS 118

RESULT 11
S21810
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S21810
R:Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
submitted to the EMBL Data Library, January 1991
A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy chain
A:Reference number: S21810
A:Accession: S21810
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <OST>
A:Cross-references: EMBL:X56936; NID:g54163; PIDN:CAA40257.1; PID:g54164
C:Introns: 15/3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 483.5; DB 2; Length 138;
Best Local Similarity 79.8%; Pred. No. 8.4e-37;
Matches 95; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNYLIEWKQRPQGQLEWIGVINPGSGGTNY 60
DB 20 QVQLQSGPELVKPGASVRIKSKASGYTFTSYIHWKQRPQGQLEWIGVINPNTKY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARD---GPFAYWGQTLTVTSA 116
DB 80 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARNYSSYGLAYWGQTLTVTSA 138

RESULT 12
S38950
Ig gamma chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S38950
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;
Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp
A:Reference number: S38950; MUID:94128242; PMID:8297501
A:Accession: S38950
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLE>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 482.5; DB 2; Length 246;
Best Local Similarity 79.5%; Pred. No. 1.9e-36;
Matches 93; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNYLIEWKQRPQGQLEWIGVINPGSGGTNY 60
DB 1 QIQQLQSGPELVKPGASVKISCKASGYTFTDYIHWKQRPQGQLEWIGVIYPGSGNTKY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDGPW--FAYWGQTLTVTSA 116
DB 61 NEKFKGKATLTVDTSSTAYMQLSLTSDSAVYFCARGKGFAMDWGQTSVTYSS 117

RESULT 13
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again:
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; proglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CH2>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 78.6%; Score 482.5; DB 2; Length 446;
Best Local Similarity 79.5%; Pred. No. 3.5e-36;
Matches 93; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNYLIEWKQRPQGQLEWIGVINPGSGGTNY 60

```
Db      1 QVLOQSGELVRPGASVKISCKASGYTFDYYHHWKQRPGELEWIGWYFGSGNTKY 60
QY      61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPW-FAYWGQGTTLTVSA 116
Db      61 NEKFKGKATLTVDTSSTAYMQLSSLTSDSAVYFCARGGKFAMDYWGQGTSTVTS 117

RESULT 14
E30562
Ig heavy chain V region (27.10.2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C/Accession: E30562
R/Sikder, S.K.; Borden, P.; Gruzso, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A/Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
A/Reference number: A30562; MUID:89110066; PMID:2464031
A/Accession: E30562
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SIK>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match      78.4%; Score 481.5; DB 2; Length 119;
Best Local Similarity 78.2%; Pred No. 1.1e-36;
Matches 93; Conservative 9; Mismatches 14; Indels 3; Gaps 1;

QY      1 QVLOQSGAELVRPGTSVKVCKASGYAFTNYLIEWVKQRPQGQLEWIGVINPGSGGTNY 60
Db      1 QVLOQSGAELMKPGASVKISCKATGYTFSSYIEWVKQRPQGHLEWIGEIFPGSGSTKY 60
QY      61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR---DGPWFAYWGQGTTLTVSA 116
Db      61 NEKFKGKATLTADTSNTAYMQLSSLTSDSAVYCARHYGSSSFAYWGQGTTLTVSA 119

RESULT 15
JL0076
Ig heavy chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C/Accession: JL0076
R/Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A/Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reac
A/Reference number: JL0076; MUID:89096973; PMID:3211160
A/Accession: JL0076
A/Molecule type: mRNA
A/Residues: 1-141 <KAA>
A/Cross-references: GB:M27788; NID:g195851; PIDN:AAA38441.1; PID:g195852
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-141/Product: Ig heavy chain #status predicted <MAT>
F/34-117/Domain: immunoglobulin homology <IMM>
F/50-54/Region: complementarity-determining 1
F/69-85/Region: complementarity-determining 2
F/123-135/Region: J2 segment
F/136-141/Region: C

Query Match      78.3%; Score 481; DB 2; Length 141;
Best Local Similarity 77.6%; Pred. No. 1.4e-36;
Matches 90; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY      1 QVLOQSGAELVRPGTSVKVCKASGYAFTNYLIEWVKQRPQGQLEWIGVINPGSGGTNY 60
Db      20 QVLOQPGAELVRPGASVKISCKASGYTFSTWVHWVKQRPQGRGLEWIGRIDPNSGGTKY 79
QY      61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPWFAYWGQGTTLTVSA 116
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Db 80 NEKFKGKATLTVDKPSSTAYMQLSSLTSDSAVYFCARGPGAGDYWGQGTTLTVSS 135

Search completed: August 16, 2004, 11:09:11
Job time : 13.4843 secs

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OM protein - protein search, using sw model

Run on: August 16, 2004, 11:08:06 ; Search time 8.32287 Seconds
(without alignments)
725.728 Million cell updates/sec

Title: US-09-889-300A-1
Perfect score: 614
Sequence: 1 QVLOQSGAELVRPCTSVKV.....ARDGFWFYWGQGLTVTUSA 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	475.5	77.4	138	1 HV48_MOUSE	P03980 mus musculus
2	471.5	76.8	120	1 HV03_MOUSE	P01747 mus musculus
3	469.5	76.5	140	1 HV02_MOUSE	P01746 mus musculus
4	466	75.9	139	1 HV01_MOUSE	P01751 mus musculus
5	457	74.4	137	1 HV11_MOUSE	P01755 mus musculus
6	455.5	74.2	117	1 HV12_MOUSE	P01756 mus musculus
7	454.5	74.0	117	1 HV13_MOUSE	P01757 mus musculus
8	454.5	74.0	121	1 HV01_MOUSE	P01745 mus musculus
9	432	70.4	120	1 HV50_MOUSE	P01745 mus musculus
10	429	69.9	117	1 HV04_MOUSE	P01748 mus musculus
11	427	69.5	117	1 HV52_MOUSE	P06327 mus musculus
12	425	69.2	118	1 HV51_MOUSE	P06330 mus musculus
13	414	67.4	117	1 HV06_MOUSE	P01750 mus musculus
14	414	67.4	117	1 HV09_MOUSE	P01753 mus musculus
15	411	66.9	117	1 HV05_MOUSE	P01749 mus musculus
16	410	66.8	117	1 HV49_MOUSE	P06328 mus musculus
17	410	66.8	117	1 HV10_MOUSE	P01754 mus musculus
18	401.5	65.4	136	1 HV15_MOUSE	P01759 mus musculus
19	385	62.7	147	1 HV1C_HUMAN	P01744 homo sapien
20	384	62.5	117	1 HV14_MOUSE	P01758 mus musculus
21	368	59.9	117	1 HV1G_HUMAN	P3083 homo sapien
22	363	59.1	117	1 HV1B_HUMAN	P01743 homo sapien
23	356	58.0	114	1 HV00_MOUSE	P01741 mus musculus
24	332.5	54.2	117	1 HV1A_HUMAN	P01742 homo sapien
25	327	53.3	122	1 HV37_HUMAN	P01768 homo sapien
26	324	52.8	119	1 HV36_MOUSE	P01807 mus musculus
27	320	52.1	119	1 HV40_MOUSE	P01810 mus musculus
28	316.5	51.5	120	1 HV3J_HUMAN	P01771 homo sapien
29	316	51.5	120	1 HV1H_HUMAN	P00421 homo sapien
30	314.5	51.2	142	1 HV01_RAT	P01805 rattus norv
31	312	50.8	119	1 HV38_MOUSE	P01808 mus musculus
32	309.5	50.4	119	1 HV3I_HUMAN	P01770 homo sapien
33	308.5	50.2	115	1 HV32_MOUSE	P01801 mus musculus

ALIGNMENTS

RESULT 1

ID	HV48_MOUSE	STANDARD	PRT	138 AA
AC	P03980;			
DT	23-OCT-1986 (Rel. 02, Created)			
DT	23-OCT-1986 (Rel. 02, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V region TEPC 1017 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84248078; PubMed=6429563;			
RA	Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,			
RA	Tucker P.W.;			
RT	"Illegitimate recombination generates a class switch from C mu to C			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984)."			
DR	PIR; A02033; HWMST7.			
DR	HSSP; P01810; 2FBJ.			
DR	InterPro; IPR007110; Ig-like.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG LIKE; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL 1 20			
FT	CHAIN 21 138			
FT	IG HEAVY CHAIN V REGION TEPC 1017.			
FT	FRAMEWORK-1.			
FT	COMPLEMENTARITY-DETERMINING-1.			
FT	FRAMEWORK-2.			
FT	COMPLEMENTARITY-DETERMINING-2.			
FT	FRAMEWORK-3.			
FT	COMPLEMENTARITY-DETERMINING-3.			
FT	FRAMEWORK-4.			
FT	BY SIMILARITY.			
FT	NON TER 138 138			
SQ	SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;			

Query Match 77.4%; Score 475.5; DB 1; Length 138;

Best Local Similarity 77.3%; Pred. No. 6.3e-43;

Matches 92; Conservative 8; Mismatches 16; Indels 3; Gaps 2;

QY 1 QVLOQSGAELVRPCTSVKVSKASGVAFNTLYLEWKQRPQGQGLEWIGVIFGSGGTNY 60

Db 20 QVLOQPGAEVLKFGASVQLSCASGHTFTNYLHWVKQRPQGQGLEWIGVIFGSGGTNY 79

QY 61 NEKFKGKATLTADKSSSTAYNQLSSLTSDSANYFCAR-DG--PWFAYWGQGLTVTUSA 116

Db 80 NEKFKATLTVDKSSSTAYNQLSSLTPEFAVYICARSDGYDFWYWCQGLTVTUSA 138

RESULT 2

HV03_MOUSE

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ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain v region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=618648;
RA Siekevitz M., Gelfand M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE. THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01789; IMCP.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin v region; Hybridoma.
FT DOMAIN 1 111
FT NON TER 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 76.8%; Score 471.5; DB 1; Length 120;
Best Local Similarity 76.7%; Pred. No. 1.4e-42;
Matches 92; Conservative 8; Mismatches 15; Indels 5; Gaps 1;

QY 2 VQLQSGAELVRPQTSVKVSKASGYAFTNYLIEWKQRPQGGLEWIGVNPQSGGTNYN 61
DB 1 VQLQSGAELVRAGSSVKMSCKASGYFTSYGINWVKQRPQGGLEWIGVNPQSGGTNYN 60
QY 62 EKFKGKATLTADKSSSTAYNQLSSLTSDSAVYFCARD-----GPWFAYWGQGLTVTVA 116
DB 61 EKFKGKATLTADKSSSTAYNQLSSLTSDSAVYFCARSVYVGGSYFYDWGQGLTVTVA 120

RESULT 3
HV02_MOUSE STANDARD; PRT; 140 AA.
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain v region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estes P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00529; AAA38170.1;
CC PIR; A90809; MHMS18.
CC PDB; 1A6U; 27-MAY-98.

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EMBL; J00493; AAA38128.1;
DR PIR; A94264; HVMSG7.
DR HSP; P01810; 2FBU.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin v region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 76.5%; Score 469.5; DB 1; Length 140;
Best Local Similarity 76.9%; Pred. No. 2.7e-42;
Matches 93; Conservative 9; Mismatches 14; Indels 5; Gaps 2;

QY 1 QVLOQSGAELVRPQTSVKVSKASGYAFTNYLIEWKQRPQGGLEWIGVNPQSGGTNY 60
DB 20 EVLOQSGAELVRAGSSVKMSCKASGYFTSYGINWVKQRPQGGLEWIGVNPQSGGTNY 79
QY 61 NEKFKGKATLTADKSSSTAYNQLSSLTSDSAVYFCARD---GPW-FAYWGQGLTVTVS 115
DB 80 NEKFKGKATLTADKSSSTAYNQLSSLTSDSAVYFCARSVYVGGSYFYDWGQGLTVTVS 139
QY 116 A 116
DB 140 S 140

RESULT 4
HV07_MOUSE STANDARD; PRT; 139 AA.
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain v region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00529; AAA38170.1;
CC PIR; A90809; MHMS18.
CC PDB; 1A6U; 27-MAY-98.
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DR PDB; 1A6W; 15-JUL-98.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4PD0C9F465 CRC64;

Query Match 75.9%; Score 466; DB 1; Length 139;
Best Local Similarity 74.2%; Pred. No. 6.3e-42;
Matches 89; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

QY 1 QVQLQQSGAELVRPGTSVKVSKASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
DB 20 QVQLQQSGAELVKPGASVKLSCKASGYFTSYLHWVWVKRPGGLEWIGRIDPNSGGTTY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSASVYFCAR---DGPWFAYWGQGLTVTVSA 116
DB 80 NEKFKSKATLTVDKPSSTAYMQLSSLTSDSASVYCYARYDYGSYFDYWGQGLTTLTVSS 139

RESULT 5
HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6789376;
RA Baltimore D.;
RA "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MGENA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
CC
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CC
CC EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; GMS43.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 74.4%; Score 457; DB 1; Length 137;
Best Local Similarity 73.7%; Pred. No. 5.5e-41;
Matches 87; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

QY 1 QVQLQQSGAELVRPGTSVKVSKASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
DB 20 QVQLQQSGAELVKPGASVKLSCKASGYFTSYLHWVWVKRPGGLEWIGRIDPNSGGTTY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSASVYFCAR---DGPWFAYWGQGLTVTVSA 116
DB 80 NEKFKSKATLTIDKPSSTAYMQLSSLTSDSASVYCYARYLGRYFDYWGQGLTTLTVSS 137

RESULT 6
HV12_MOUSE STANDARD; PRT; 117 AA.
ID HV12_MOUSE
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 1045.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=8307344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RA "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
PROTEIN HAS ALSO BEEN DETERMINED.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT CARCCHVD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 74.2%; Score 455.5; DB 1; Length 117;
Best Local Similarity 73.5%; Pred. No. 6.5e-41;
Matches 86; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLQQSGAELVRPGTSVKVSKASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
DB 1 EVQLQQSGPELVKPGASVKMSCKASGYFTFDYMKWKYQSHGKSLIEWIGDINFGNGGTSY 60

```
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPW-FAYWQGGTLVTYSA 116
RL :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYCARDYDWFVWVGAGTIVTSS 117

RESULT 7
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RA MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -|- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -|- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 74.0%; Score 454.5; DB 1; Length 117;
Best Local Similarity 73.5%; Pred. No. 8.3e-41;
Matches 86; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVPGTSVKVKSCASGYAFITNYLIEWKQRPQGLEWIGVINPGSGGTNY 60
DB 1 EVQLQSGPELVKPGASVKMSCKASGYTFTDYMKWVKQSHGKSLIEWIGDINPNNGGTSY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPW-FAYWQGGTLVTYSA 116
RL :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYCARDYDWFVWVGAGTIVTSS 117

RESULT 8
HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
[2]
RN REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -|- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93708; GVM511.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56BD0BF CRC64;

Query Match 74.0%; Score 454.5; DB 1; Length 121;
Best Local Similarity 71.9%; Pred. No. 8.7e-41;
Matches 87; Conservative 11; Mismatches 18; Indels 5; Gaps 1;

QY 1 QVQLQSGAELVPGTSVKVKSCASGYAFITNYLIEWKQRPQGLEWIGVINPGSGGTNY 60
DB 1 EAQLQSGAELVPGTSVKISKAGYFTFTNYWGWKRGHGLEWIGDIYPGGGFTNY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR----DGPWFYWGQGLTVTVS 115
RL :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 NDNLKGKATLTADTSSSTAYIQLSLSLTSEDSAIYHCARGIYNSPYSFDSWGQGLTVTVS 120

QY 116 A 116
DB 121 S 121

RESULT 9
HV50_MOUSE
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=64182519; PubMed=6201362;
RX Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 70.4%; Score 432; DB 1; Length 120;
Best Local Similarity 69.2%; Pred. No. 2e-38;
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Matches 83; Conservative 13; Mismatches 20; Indels 4; Gaps 2;
QY 1 QVQLQSGAELVRPQTSVKVSKASGYAFTNYLIEWVKQRPQGQLEWIGVINPGSGGTNY 60
DB 1 QVQLQSGTELVPKASVNLKSKASGYFTTSYWHWIRQRPQGQLEWIGVINPGSGGTNY 60
QY 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSNAVYFCAR---DGP-WFAYWGQGLTVTUSA 116
DB 61 NEKFKSKATLTVDKSSSATYMQSLTPTSDSNAVYCARWYEGDRYDVGTTVTVSS 120

RESULT 10
HV04 MOUSE
ID HV04 MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RC Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR; A02030; HVM823.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 69.9%; Score 429; DB 1; Length 117;
Best Local Similarity 81.6%; Pred. No. 3.9e-38;
Matches 80; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
QY 1 QVQLQSGAELVRPQTSVKVSKASGYAFTNYLIEWVKQRPQGQLEWIGVINPGSGGTNY 60
DB 20 QVQLQSGTELVPKASVNLKSKASGYFTTSYWHWIRQRPQGQLEWIGVINPGSGGTNY 79
QY 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSNAVYFCAR 98
DB 80 NEKFKSKATLTVDKSSSATYMQSLTPTSDSNAVYCAR 117

RESULT 11
HV52 MOUSE
ID HV52 MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
```

```
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=8509340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; M13787; AAA38499.1; -.
DR PIR; A02029; HVM8A1.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 69.5%; Score 427; DB 1; Length 117;
Best Local Similarity 83.7%; Pred. No. 6.4e-38;
Matches 82; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 QVQLQSGAELVRPQTSVKVSKASGYAFTNYLIEWVKQRPQGQLEWIGVINPGSGGTNY 60
DB 20 QVQLQSGTELVPKASVNLKSKASGYFTTSYWHWIRQRPQGQLEWIGVINPGSGGTNY 79
QY 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSNAVYFCAR 98
DB 80 NEKFKSKATLTVDKSSSATYMQSLTPTSDSNAVYFCAR 117

RESULT 12
HV51 MOUSE
ID HV51 MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
```

DR PIR: A02040; MHMS38.
 DR HSP: P01789; IMCP.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Ig; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 98 V SEGMENT.
 FT DOMAIN 99 104 D SEGMENT.
 FT DOMAIN 105 118 J SEGMENT.
 FT DISULFID 22 96 BY SIMILARITY.
 FT NON TER 118 118
 SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
 Query Match 69.2%; Score 425; DB 1; Length 118;
 Best Local Similarity 68.6%; Pred. No. 18-37; Indels 2; Gaps 1;
 Matches 81; Conservative 14; Mismatches 21; Indels 2; Gaps 1;
 Qy 1 QVQLQSGAEELVRPGTSVKVSKASGYAFTNYLIEWKQRPQGGLWIGVINPGSGGTNY 60
 Db 1 EVQLQSGPELVKPGASVKISCKASGYTFTDYMMWVQSHGKSLWIGDINPNNGGTSY 60
 Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDGPW--PAYWQGLTYTVSA 116
 Db 61 NQKFKGKATLTVDKSSSATYMLRSLTSDSAVYFCARGYGYDPFDVWGTVGTVTVSS 118
 RESULT 13
 HV06_MOUSE
 ID HV06_MOUSE STANDARD; PRT; 117 AA.
 AC P01750;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 102 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RA "Heavy chain variable region contribution to the Npb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 CC PIR: A02032; HVM502.
 DR HSP: P01810; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Ig; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;
 Query Match 67.4%; Score 414; DB 1; Length 117;
 Best Local Similarity 81.2%; Pred. No. 15e-36;
 Matches 78; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
 Qy 1 QVQLQSGAEELVRPGTSVKVSKASGYAFTNYLIEWKQRPQGGLWIGVINPGSGGTNY 60
 Db 1 EVQLQSGPELVKPGASVKISCKASGYTFTDYMMWVQSHGKSLWIGDINPNNGGTSY 60
 Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDGPW--PAYWQGLTYTVSA 116
 Db 61 NQKFKGKATLTVDKSSSATYMLRSLTSDSAVYFCARGYGYDPFDVWGTVGTVTVSS 118
 RESULT 14
 HV09_MOUSE
 ID HV09_MOUSE STANDARD; PRT; 117 AA.
 AC P01753; P11271;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 186-1 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RA "Heavy chain variable region contribution to the Npb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 CC PIR: D90809; HVM561.
 DR HSP: P01810; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Ig; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;
 Query Match 67.4%; Score 414; DB 1; Length 117;
 Best Local Similarity 79.6%; Pred. No. 1.5e-36;
 Matches 78; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
 Qy 1 QVQLQSGAEELVRPGTSVKVSKASGYAFTNYLIEWKQRPQGGLWIGVINPGSGGTNY 60
 Db 20 QVQLQSGAEELVRPGTSVKVSKASGYTFTSYMMHWKQRPGRGLEWIGRIDPNSGTTY 79
 Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCAR 98
 Db 80 NEKFKGKATLTVDTSSTAYMQLSLTSDSAVYFCAR 117
 RESULT 15
 HV05_MOUSE
 ID HV05_MOUSE STANDARD; PRT; 117 AA.
 AC P01749;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig heavy chain V region 3 precursor.

Qy 2 VQLQSGAEELVRPGTSVKVSKASGYAFTNYLIEWKQRPQGGLWIGVINPGSGGTNY 61
 Db 21 VQLQSGAEELVRPGTSVKVSKASGYTFTSYMMHWKQRPGRGLEWIGRIDPNSDNTYN 80
 Qy 62 ERFKKGKATLTADKSSSTAYMQLSLTSDSAVYFCA 97
 Db 81 QRFKKGKATLTVDKSSSTAYMQLSLTSDSAVYFCA 116

Search completed: August 16, 2004, 11:08:35
Job time : 8.32287 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 16, 2004, 11:08:06 ; Search time 34.3318 seconds
(without alignments)
1066.069 Million cell updates/sec

Title: US-09-889-300A-1

Perfect score: 614

Sequence: 1 QVQLQQSGAEIVRPGTSVKV.....ARDGPNFAYWGQGLTVTSA 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*

1: sp.archaea.*

2: sp.bacteria.*

3: sp.fungi.*

4: sp.human.*

5: sp.invertebrate.*

6: sp.mammal.*

7: sp.mhc.*

8: sp.organelle.*

9: sp.phase.*

10: sp.plant.*

11: sp.rodent.*

12: sp.virus.*

13: sp.vertebrate.*

14: sp.unclassified.*

15: sp.virus.*

16: sp.bacteriap.*

17: sp.archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	526.5	85.7	473	11 Q9D8L4	Q9D8L4 mus musculus
2	484.5	78.9	614	11 Q7TM6	Q7TM6 mus musculus
3	483.5	78.7	142	11 Q924Q1	Q924Q1 mus musculus
4	477	77.7	463	11 Q99LC4	Q99LC4 mus musculus
5	475	77.4	143	11 Q924Q0	Q924Q0 mus musculus
6	472.5	77.0	481	11 Q91WT1	Q91WT1 mus musculus
7	471	76.7	482	11 Q9K172	Q9K172 mus musculus
8	470.5	76.6	489	11 Q9VCX4	Q9VCX4 mus musculus
9	470	76.5	145	11 Q924P7	Q924P7 mus musculus
10	468	76.2	613	11 Q9VCX7	Q9VCX7 mus musculus
11	467	76.1	141	11 Q924Q4	Q924Q4 mus musculus
12	466.5	76.0	140	11 Q924P8	Q924P8 mus musculus
13	466	75.9	145	11 Q924C7	Q924C7 mus musculus
14	466	75.9	145	11 Q924D1	Q924D1 mus musculus
15	466	75.9	145	11 Q924E1	Q924E1 mus musculus
16	463	75.4	139	11 Q924R5	Q924R5 mus musculus

17	462.5	75.3	146	11 Q924R8	Q924R8 mus musculus
18	462.5	75.3	480	11 Q8K0Z4	Q8K0Z4 mus musculus
19	462	75.2	143	11 Q924R0	Q924R0 mus musculus
20	461	75.1	137	11 Q924R6	Q924R6 mus musculus
21	461	75.1	145	11 Q924Q6	Q924Q6 mus musculus
22	460.5	75.0	146	11 Q924Q8	Q924Q8 mus musculus
23	460	74.9	143	11 Q924Q5	Q924Q5 mus musculus
24	460	74.9	143	11 Q91V67	Q91V67 mus musculus
25	460	74.9	145	11 Q924Q9	Q924Q9 mus musculus
26	458.5	74.7	117	11 Q90XF0	Q90XF0 mus musculus
27	458.5	74.7	146	11 Q924Q3	Q924Q3 mus musculus
28	458	74.6	278	11 Q924K1	Q924K1 mus musculus
29	457.5	74.5	140	11 Q924R2	Q924R2 mus musculus
30	457	74.4	118	11 Q921C4	Q921C4 mus musculus
31	457	74.4	145	11 Q924R4	Q924R4 mus musculus
32	456	74.3	481	11 Q8VCV5	Q8VCV5 mus musculus
33	453.5	73.9	117	11 Q90XE9	Q90XE9 mus musculus
34	453.5	73.9	144	11 Q924P5	Q924P5 mus musculus
35	453	73.8	473	11 Q99L25	Q99L25 mus musculus
36	452	73.6	143	11 Q924R7	Q924R7 mus musculus
37	449	73.1	109	11 Q9JL75	Q9JL75 mus musculus
38	449	73.1	143	11 Q924P9	Q924P9 mus musculus
39	448.5	73.0	120	11 Q920B8	Q920B8 mus musculus
40	447	72.8	143	11 Q91VA2	Q91VA2 mus musculus
41	446.5	72.7	168	11 Q8VDC9	Q8VDC9 mus musculus
42	445.5	72.6	123	11 Q8VIJ1	Q8VIJ1 mus musculus
43	445	72.5	488	11 Q91WR1	Q91WR1 mus musculus
44	442	72.0	136	11 Q7TPE3	Q7TPE3 mus musculus
45	438	71.3	143	11 Q924P6	Q924P6 mus musculus

ALIGNMENTS

RESULT 1	
Q9D8L4	
ID Q9D8L4	PRELIMINARY; PRT: 473 AA.
AC Q9D8L4	
DT 01-JUN-2001 (TRENBLrel. 17, Created)	
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)	
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)	
DE 1810060009Rik protein.	
GN IGH-1 OR 1810060009RIK.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX NCBI_TaxID=10090;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=C57BL/6J; TISSUE=Pancreas;	
RX MEDLINE=21085660; PubMed=11217851;	
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,	
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,	
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,	
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,	
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,	
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,	
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,	
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,	
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,	
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,	
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,	
RA Gustingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,	
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,	
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,	
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,	
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,	
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,	
RA Hayashizaki Y.;	
RT "Functional annotation of a full-length mouse cDNA collection.";	
RL Nature 409:685-690(2001).	
DR EMBL; AK007918; BAB25349.1; --	
DR FIR; S26746; S26746.	

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DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR031006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SMC0406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 85.7%; Score 526.5; DB 11; Length 473;
Best Local Similarity 84.9%; Pred. No. 2.5e-46;
Matches 10; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

Qy 1 QVQLQSGAEIVRPQTISKVSKASGYAFTNLYIEWKQRPQGLEWIGVINPGSGGTNY 60
Db 20 QVQLQSGAEIVRPQTISKVSKASGYAFTNLYIEWKQRPQGLEWIGVINPGSGGTNY 79

Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDG---PWFAYWGQGLTVTVA 116
Db 80 NGKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDYGSRYFAYWGQGLTVTVA 138

Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDG---PWFAYWGQGLTVTVA 116
Db 80 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARSGYDYDFAYWGQGLTVTVA 138

RESULT 2
Q7TWT6 PRELIMINARY; PRT; 614 AA.
ID Q7TWT6 STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
AC Q7TWT6 MEDLINE=22388257; PubMedID=12477932;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP Strausberg R.;
RA Strausberg R.;

Query Match 78.9%; Score 484.5; DB 11; Length 614;
Best Local Similarity 79.8%; Pred. No. 8.3e-42;
Matches 95; Conservative 8; Mismatches 13; Indels 3; Gaps 1;

Qy 1 QVQLQSGAEIVRPQTISKVSKASGYAFTNLYIEWKQRPQGLEWIGVINPGSGGTNY 60
Db 20 QVQLQSGAEIVRPQTISKVSKASGYAFTNLYIEWKQRPQGLEWIGVINPGSGGTNY 79

Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDG---PWFAYWGQGLTVTVA 116
Db 80 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARSGYDYDFAYWGQGLTVTVA 138

RESULT 3
Q924Q1 PRELIMINARY; PRT; 142 AA.
ID Q924Q1 STRAIN=C57BL/6;
AC Q924Q1 STRAIN=C57BL/6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP Strausberg R.;
RA Strausberg R.;

Query Match 78.7%; Score 483.5; DB 11; Length 142;
Best Local Similarity 79.7%; Pred. No. 1.6e-42;
Matches 94; Conservative 8; Mismatches 13; Indels 3; Gaps 2;

Qy 1 QVQLQSGAEIVRPQTISKVSKASGYAFTNLYIEWKQRPQGLEWIGVINPGSGGTNY 60
Db 1 QVQLQSGAEIVRPQTISKVSKASGYAFTNLYIEWKQRPQGLEWIGVINPGSGGTNY 60

Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGFWFA--YWGQGLTVTVA 116
Db 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARRG--WEANDYWGQGLTVTVA 117

RESULT 4
Q99LC4 PRELIMINARY; PRT; 463 AA.
ID Q99LC4 STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
AC Q99LC4 MEDLINE=22388257; PubMedID=12477932;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 181060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP Strausberg R.;
RA Strausberg R.;

Query Match 78.9%; Score 484.5; DB 11; Length 614;
Best Local Similarity 79.8%; Pred. No. 8.3e-42;
Matches 95; Conservative 8; Mismatches 13; Indels 3; Gaps 1;

Qy 1 QVQLQSGAEIVRPQTISKVSKASGYAFTNLYIEWKQRPQGLEWIGVINPGSGGTNY 60
Db 20 QVQLQSGAEIVRPQTISKVSKASGYAFTNLYIEWKQRPQGLEWIGVINPGSGGTNY 79

Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGFWFA--YWGQGLTVTVA 116
Db 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARRG--WEANDYWGQGLTVTVA 117

RESULT 4
Q99LC4 PRELIMINARY; PRT; 463 AA.
ID Q99LC4 STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
AC Q99LC4 MEDLINE=22388257; PubMedID=12477932;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 181060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP Strausberg R.;
RA Strausberg R.;

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RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC003435; AAH03435.1; -.
DR PIR; B45837; B45837.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 77.7%; Score 477; DB 11; Length 463;
Best Local Similarity 77.5%; Pred. No. 3.5e-41;
Matches 93; Conservative 7; Mismatches 16; Indels 4; Gaps 1;

QY 1 QVQLQSGAELVPGTSVKVSKASGYAFTNVLIEWVKQRPQGQLEWIGVINPGSGGTNY 60
DB 20 QVQLQSGAELARPGASVRLSKASGYFTGTGYSWVKQRTGQGLEWVGELYPGSGNTYY 79
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPW----PAYWGQGLTVTSA 116
DB 80 SEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPW----PAYWGQGLTVTSA 139

RESULT 5

Q924Q0 Q924Q0 PRELIMINARY; PRT; 143 AA.

AC Q924Q0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE V165-D-J-C mu protein (fragment).
GN V165-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;

RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB069915; BAB63931.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15704 MW; C99D243F2BAD8A0 CRC64;

Query Match 77.4%; Score 475; DB 11; Length 143;
Best Local Similarity 78.0%; Pred. No. 1.3e-41;
Matches 92; Conservative 8; Mismatches 16; Indels 2; Gaps 1;

QY 1 QVQLQSGAELVPGTSVKVSKASGYAFTNVLIEWVKQRPQGQLEWIGVINPGSGGTNY 60
DB 1 QVQLQSGAELVPGASVRLSKASGYFTGTGYSWVKQRTGQGLEWIGDIYPGSGGTNY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGP--WPAYWGQGLTVTSA 116
DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDPSNHLFDYWGQGLTVTSS 118

RESULT 6

Q91WT1

ID Q91WT1 PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 77.0%; Score 472.5; DB 11; Length 481;

Best Local Similarity 77.8%; Pred. No. 1.1e-40;
Matches 91; Conservative 6; Mismatches 19; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVPGTSVKVSKASGYAFTNVLIEWVKQRPQGQLEWIGVINPGSGGTNY 60
DB 20 QVQLQSGPELVKPGASVKISKASGYFTTSYIHWVKQRPQGQLVWIGWYPCDGNTRY 79
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPW--PAYWGQGLTVTSA 116
DB 80 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCRTGGWAFDYWGQGLTVTSS 136

RESULT 7

O8K172 O8K172 PRELIMINARY; PRT; 482 AA.

AC O8K172;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to expressed sequence AI893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028249; AAH28249.1; -.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.

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DR PIR; PH1152; PH1153.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
SQ SEQUENCE 482 AA; 52121 MW; A06FF083E771D084 CRC64;

Query Match 76.8%; Score 471; DB 11; Length 482;
Best Local Similarity 76.8%; Pred. No. 1.6e-40;
Matches 90; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

QY 1 QVQLQQSGAELVPGTSTVKVSKASGYAFTNLYLIEWVKORPGQGLEWIGVINPQSGGTNY 60
DB 20 QVQLQQSGAELVPGASVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGRIDPNSSGGTKY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSLSLSDSAVYFCAR--YWGQGLTVTVA 116
DB 80 NEKFKSKATLTVDKPSSTAYMQLSLSLSDSAVYCTREGDYDAMDYWGQGSTVTSS 137

RESULT 8
Q8VCX4 PRELIMINARY; PRT; 489 AA.
AC Q8VCX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-VJ558 OR A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018322; AAH18322.1; -.
DR MGI; MGI:96486; IGH-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 489 AA; 53208 MW; CC85B1194DAF8F2C CRC64;

Query Match 76.8%; Score 470.5; DB 11; Length 489;
Best Local Similarity 72.8%; Pred. No. 1.8e-40;
Matches 91; Conservative 9; Mismatches 16; Indels 9; Gaps 2;

QY 1 QVQLQQSGAELVPGTSTVKVSKASGYAFTNLYLIEWVKORPGQGLEWIGVINPQSGGTNY 60
DB 20 QVQLQQSGAELVPGASVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGVINPQSGGSIKF 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSLSLSDSAVYFCAR-----DG--PMFAYWGQGLT 111
DB 80 NEKFKDKATLTADKSSSTVYMDLSRLTSDSAVYFCARHEDRGNVDGSLANFVYWGQGLT 139

QY 112 VTVSA 116
DB 140 VTVSA 144
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RESULT 9
Q924P7 PRELIMINARY; PRT; 145 AA.
AC Q924P7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS069918; BAB63934.1; -.
DR PIR; F28833; F28833.
DR PIR; F39332; F39332.
DR PIR; PH1105; PH1105.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1142; PH1142.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 145
SQ SEQUENCE 145 AA; 15988 MW; FB73958704796C9A CRC64;

Query Match 76.5%; Score 470; DB 11; Length 145;
Best Local Similarity 77.5%; Pred. No. 4.3e-41;
Matches 93; Conservative 9; Mismatches 14; Indels 4; Gaps 2;

QY 1 QVQLQQSGAELVPGTSTVKVSKASGYAFTNLYLIEWVKORPGQGLEWIGVINPQSGGTNY 60
DB 1 QVQLQQGAELVPGSSVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGRIDPNSSGGTKY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSLSLSDSAVYFCAR-DGPWF---AYWGQGLTVTVA 116
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLSLSDSAVYFCAR--YWGQGLTVTVA 120

RESULT 10
Q8VCX7 PRELIMINARY; PRT; 613 AA.
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RN  SEQUENCE FROM N.A.
RP  TISSUE-Salivary gland;
RA  Strausberg R.;
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; SC019315; RAH19315.1; -.
DR  MGD; MGI:96448; Igh-6.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; IG_V.
DR  Pfam; PF00047; Ig; 5.
DR  SMART; SM00406; Igv; 1.
DR  PROSITE; PS08335; IG_LIKE; 5.
DR  PROSITE; PS00290; IG_MHC; 3.
DR  Hypothetical protein.
KW  SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match          76.2%; Score 468; DB 11; Length 613;
Best Local Similarity 77.1%; Pred. No. 4.3e-40;
Matches 91; Conservative 10; Mismatches 15; Indels 2; Gaps 2;

QY  1 QVQLQSGAELVRPGTSVKVSKASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db  20 QVQLQSGAELMKPGASVKISKATGYTFSSYWIWVKRPGHGLEWIGILPGSGSTNY 79

QY  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSDSAVYFCARD-GPW-FAYWGQGLTVTUSA 116
Db  80 NEKFKGKATFTADTSNTAYMQLSSLTSEDSAVYICARLGRWTFDVGAGTTLTVSS 137

RESULT 11
Q924Q4 PRELIMINARY; PRT; 141 AA.
ID Q924Q4;
AC Q924Q4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067796; BAB63281.1; -.
DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.


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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS08335; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 141
SQ SEQUENCE 141 AA; 15561 MW; DDD80482D66B76A0 CRC64;

Query Match          76.1%; Score 467; DB 11; Length 141;
Best Local Similarity 75.9%; Pred. No. 8.5e-41;
Matches 88; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY  1 QVQLQSGAELVRPGTSVKVSKASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db  1 QVQLQPGAELVRFGASVKLSCKASGYTFSTYSYWHWVKRPGQGLEWIGRIDNSGTTY 60

QY  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSDSAVYFCARDGFW-FAYWGQGLTVTUSA 116
Db  61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYICARDYDGRFTWGQGLTLTVSS 116

RESULT 12
Q924P8 PRELIMINARY; PRT; 140 AA.
ID Q924P8;
AC Q924P8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN V23-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069917; BAB63933.1; -.
DR PIR; I28833; I28833.
DR PIR; PH1156; PH1156.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS08335; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 15392 MW; 904C80C82548C936 CRC64;

Query Match          76.0%; Score 466.5; DB 11; Length 140;
Best Local Similarity 76.9%; Pred. No. 9.5e-41;
Matches 90; Conservative 10; Mismatches 14; Indels 3; Gaps 2;

QY  1 QVQLQSGAELVRPGTSVKVSKASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db  1 QVQLQPGTGLVKPGASVKLSCKASGYTFSTYSYWHWVKRPGQGLEWIGINPSNGTNY 60

QY  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSDSAVYFCARDGFW-FAYWGQGLTVTUSA 116
Db  61 NEKFKSKATLTVDKSSSTACTQLSLSLTSEDSAVYICARN--WDPDYWGQGLTLTVSS 115

RESULT 13
Q924R3 PRELIMINARY; PRT; 145 AA.
ID Q924R3;
AC Q924R3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)


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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE VHL86.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067787; BAB63272.1; -;
 DR PIR; F28833; F28833.
 DR PIR; PH1105; PH1105.
 DR PIR; PH1108; PH1108.
 DR PIR; PH1114; PH1114.
 DR PIR; PH1118; PH1118.
 DR PIR; PH1119; PH1119.
 DR PIR; PH1125; PH1125.
 DR PIR; PH1126; PH1126.
 DR PIR; PH1128; PH1128.
 DR PIR; PH1129; PH1129.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1134; PH1134.
 DR PIR; PH1137; PH1137.
 DR PIR; PH1139; PH1139.
 DR PIR; PH1142; PH1142.
 DR PIR; PH1144; PH1144.
 DR PIR; PH1147; PH1147.
 DR PIR; PH1149; PH1149.
 DR PIR; PH1150; PH1150.
 DR PIR; PH1151; PH1151.
 DR PIR; PH1152; PH1152.
 DR PIR; PH1153; PH1153.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON TER 1
 FT NON TER 145
 SQ SEQUENCE 145 AA; 15996 MW; 35B1A36E4280BA81 CRC64;
 Query Match 75.9%; Score 466; DB 11; Length 145;
 Best Local Similarity 75.8%; Pred. No. 1.1e-40;
 Matches 91; Conservative 9; Mismatches 16; Indels 4; Gaps 2;
 QY 1 QVQLQSGAEIVPGTSVKVSKASGYAFTNYLIEWVKQPGQGLEWIGVINGSGGTNY 60
 Db 1 QVQLQQGAEIVAPGASVKLSKASGYTFTSYWVHWVKQPGRGLEWIGRIDPSNGGTY 60
 QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR---DGPW-FAYWQGTLTVSA 116
 Db 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYCARGLYDGNWYFDWVGTTVTSS 120
 RESULT 14
 QY24Q7 ID Q24Q7 PRELIMINARY; PRT; 145 AA.
 AC Q24Q7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE VHL86.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067793; BAB63278.1; -;
 DR PIR; F28833; F28833.
 DR PIR; PH1105; PH1105.
 DR PIR; PH1108; PH1108.
 DR PIR; PH1114; PH1114.
 DR PIR; PH1118; PH1118.
 DR PIR; PH1119; PH1119.
 DR PIR; PH1125; PH1125.
 DR PIR; PH1126; PH1126.
 DR PIR; PH1128; PH1128.
 DR PIR; PH1129; PH1129.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1134; PH1134.
 DR PIR; PH1137; PH1137.
 DR PIR; PH1139; PH1139.
 DR PIR; PH1142; PH1142.
 DR PIR; PH1144; PH1144.
 DR PIR; PH1147; PH1147.
 DR PIR; PH1149; PH1149.
 DR PIR; PH1150; PH1150.
 DR PIR; PH1151; PH1151.
 DR PIR; PH1152; PH1152.
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 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
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 SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;
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 Best Local Similarity 74.2%; Pred. No. 1.1e-40;
 Matches 89; Conservative 11; Mismatches 16; Indels 4; Gaps 1;
 QY 1 QVQLQSGAEIVPGTSVKVSKASGYAFTNYLIEWVKQPGQGLEWIGVINGSGGTNY 60
 Db 1 QVQLQQGAEIVAPGASVKLSKASGYTFTSYWVHWVKQPGRGLEWIGRIDPSNGGTY 60
 QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR---DGPW-FAYWQGTLTVSA 116
 Db 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYCARDYVYGGSYEDYWGQGTTLTVSS 120
 RESULT 15
 QY24R1 ID Q24R1 PRELIMINARY; PRT; 145 AA.
 AC Q24R1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE VHL86.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AB067789; BAB63274.1; -.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
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DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
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DR PIR; PH1128; PH1128.
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DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;

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Best Local Similarity 76.7%; Pred. No. 1.1e-40;
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QY 1 QVQLQSGAEIVRPGTSVKVCKASGYAFTNVLIEWVKQRPQGLEWIGVINPGSGGTNY 60
Db 1 QVQLQSGAEIVRPGTSVKVCKASGYAFTNVLIEWVKQRPQGLEWIGVINPGSGGTNY 60

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Db 61 NEKFKGKATLTVDKPSSTAYMQLSSLTSDSAVYFCAR-DGFWF---AYWGQGTLTVSA 120

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